

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1713	100.0	1713	6	AX644347	AX644347	Sequence
2	1692.8	98.8	1785	6	AX747274	AX747274	Sequence
3	1692.8	98.8	1785	8	AK091952	AK091952	Homo sapi
4	1620.2	94.6	1679	8	BC033143	BC033143	Homo sapi
5	1602.4	93.5	1977	6	AX535029	AX535029	Sequence
6	1602.4	93.5	1977	6	AX535090	AX535090	Sequence
7	1197	69.9	1197	6	CQ171675	CQ171675	Sequence
8	1039	60.5	140207	8	AL356380	AL356380	Homo sapi
9	1035.8	60.5	111738	14	AL592304	AL592304	Homo sapi
10	962.8	56.2	1680	9	BC006980	BC006980	Mus muscu
11	935.8	54.6	1718	9	BC079148	BC079148	Rattus nor
12	791	46.2	193813	9	AL627228	AL627228	Mouse DN
13	773.4	45.1	235419	14	AC095979	AC095979	Rattus nor
14	773.4	45.1	249406	14	AC118963	AC118963	Rattus nor
15	773.4	45.1	256017	14	AC126312	AC126312	Rattus nor
16	463.2	27.0	728	6	BD216745	BD216745	Novel hum
17	385	22.2	385	6	AX535028	AX535028	Sequence
18	380.2	22.2	386	6	AX644346	AX644346	Sequence

DB

21 CGCACCCGTAGACCAGAC

131

121 CGCACCGTAGACCAGACCCCAAGGACCTGGCCACCATGGGCCAGAGACATTACCTTC 180

Db	210	CGCACCCGTAGACAGACCCCAAGACCCCTGGCCACCATGGCCAGAGAGCAITTAACCTTC	269
Qy	181	ATCTCTGGCTCTGCTGAGCCCGGCCCTTGAGTCCCCACCTGCTGCTGCTCTGCGGACCC	240
Db	270	ATCTCTGGCTCTGCTGAGCCCGGCCCTTGAGTCCCCACCTGCTGCTGCTCTGCGGACCC	329
Qy	241	TGGGTGTGGAGTGGTGGCCGGCTGCTTTCCTTTCCTGCTTTCGCGCTGCGCGGATTTGCTCCAG	300
Db	330	TGGGTGTGGAGTGGTGGCCGGCTGCTTTCCTTTCCTGCTTTCGCGCTGCGCGGATTTGCTCCAG	389
Qy	301	CGCTGTGGAGCTGTGTGGGGGATGCAGCCCTGCTGCTTCTACTGTAGGACTCCACCTGAG	360
Db	390	CGCTGTGGAGCTGTGTGGGGGATGCAGCCCTGCTGCTTCTACTGTAGGACTCCACCTGAG	449
Qy	361	GGGACTGTCTAAGCCAACTGGGCCAAAGAGACAAATGGAGTGGCCCCCAGCGCCTGATCGT	420
Db	450	GGGACTGTCTAAGCCAACTGGGCCAAAGAGACAAATGGAGTGGCCCCCAGCGCCTGATCGT	509
Qy	421	GCACCCCCAGCCGGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGAGCAGCTTCAGC	480
Db	510	GCACCCCCAGCCGGCGGGATGGCCAGCGCTCAAGTCAACCATGGGAGCAGCTTCAGC	569
Qy	481	TACCCCGATGTTAAGCTCAAGGCGATCCCTGTGTATCCCTACCCGAGGGGCCACCTCCCCA	540
Db	570	TACCCCGATGTTAAGCTCAAGGCGATCCCTGTGTATCCCTACCCGAGGGGCCACCTCCCCA	629
Qy	541	GCCCTCATGTGGGACTCTGCTGCAAGGAGCCACTGGCCGATCCCCACCCATCGCACAC	600
Db	630	GCCCTCATGTGGGACTCTGCTGCAAGGAGCCACTGGCCGATCCCCACCCATCGCACAC	689
Qy	601	AGCTGCCACGACACTTTTGGCAGTAGTCTCGTGGCTCCGAGGAGTACTATTTTTCAT	660
Db	690	AGCTGCCACGACACTTTTGGCAGTAGTCTCGTGGCTCCGAGGAGTACTATTTTTCAT	749
Qy	661	GAGTCCGACCTGGACCTGCCGAGATGGGCGAGTGGCTCCATGTTCGAGCCGAGAAATTGAT	720
Db	750	GAGTCCGACCTGGACCTGCCGAGATGGGCGAGTGGCTCCATGTTCGAGCCGAGAAATTGAT	809
Qy	721	GTGCTCATCTTCAAGAAAGCTGCACAGAGCTGTTTCAGCGGTACACCAAGATCGATGAGCTGGCC	780
Db	810	GTGCTCATCTTCAAGAAAGCTGCACAGAGCTGTTTCAGCGGTACACCAAGATCGATGAGCTGGCC	869
Qy	781	AAGTGCACTACAGACACTGTGTTCTCGAGAGAACCCAGTAAGATCTCGGACCTTATCAGC	840
Db	870	AAGTGCACTACAGACACTGTGTTCTCGAGAGAACCCAGTAAGATCTCGGACCTTATCAGC	929
Qy	841	AGCATCAGCAGGACTACGACTGGATGAGCAGAGATGCTGAGGCGCGCTGGTACGCGGC	900
Db	930	AGCATCAGCAGGACTACGACTGGATGAGCAGAGATGCTGAGGCGCGCTGGTACGCGGC	989
Qy	901	ATCATTCGCATTAGTATCCGAAGAGCCGTGCTCGCCACAGACCTCGGAGGGTCTTCA	960
Db	990	ATCATTCGCATTAGTATCCGAAGAGCCGTGCTCGCCACAGACCTCGGAGGGTCTTCA	1049
Qy	961	ACTCGGCTGTGCCCCAAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGC	1020
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Qy	1021	TCAGGTTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC	1080
Db	1110	TCAGGTTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC	1169
Qy	1081	ATGCCCAGGAGCTGAGCGCTTATGGAGCTCCAGGTTACCCAGCAAGCCATGACTCATCC	1140
Db	1170	ATGCCCAGGAGCTGAGCGCTTATGGAGCTCCAGGTTACCCAGCAAGCCATGACTCATCC	1229
Qy	1141	TTCCAGGGCACCGACACAGACTCGTCCGGGGCACCTTGTCTCAGGTGTACTGCTTAACCC	1200
Db	1230	TTCCAGGGCACCGACACAGACTCGTCCGGGGCACCTTGTCTCAGGTGTACTGCTTAACCC	1289
Qy	1201	CTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAAGACATGGCCTACAGAAATGAAGGG	1260

Db	1290	CTGCCAGGCCAGCTGCGCCACACCCCTTCTCGGAGAGACATGGCCCTACAGAAATGAAGAGG	1349
Qy	1261	GGACACAGGAACCCCTGTGGGAGAGGCTTAGACCTGGAAGCAGTGCCTCCTCTGGCTCCTCC	1320
Db	1350	GGACACAGGAACCCCTGTGGGAGAGGCTTAGACCTGGAAGCAGTGCCTCCTCTGGCTCCTCC	1409
Qy	1321	TGCTTGGCTGACTGGGTTCTCTGGAACATGTGCATTTTCACTGGGCCATGGATCTACATC	1380
Db	1410	TGCTTGGCTGACTGGGTTCTCTGGAACATGTGCATTTTCACTGGGCCATGGATCTACATC	1469
Qy	1381	TCCTTGCATCCCGAGCTGCTGATCCCTGCCAGGGCCCTTCTCTCTCTCTCATGTGCT	1440
Db	1470	TCCTTGCATCCCGAGCTGCTGATCCCTGCCAGGGCCCTTCTCTCTCTCTCATGTGCT	1529
Qy	1441	TCAGGTGGCCCTGATCATGGAAGTAAGGAGTTAGGCATTAACCTTCTGGGAGTGAACCCCTG	1500
Db	1530	TCAGGTGGCCCTGATCATGGAAGTAAGGAGTTAGGCATTAACCTTCTGGGAGTGAACCCCTG	1589
Qy	1501	ACTCCATCCCTTATTGGCCACCTTAACCAATCATGAAACTTCTCTCTCTCTGGGGTAAT	1566
Db	1590	ACTCCATCCCTTATTGGCCACCTTAACCAATCATGAAACTTCTCTCTCTCTGGGGTAAT	1649
Qy	1561	TCAACAGTTAAAGAGCTTATCTTAAATGATTTGATTTGGGGGGTGGGAGGGCCCACT	1620
Db	1650	TCAACAGTTAAAGAGCTTATCTTAAATGATTTGATTTGGGGGGTGGGAGGGCCCACT	1709
Qy	1621	CTATGTTATCTTAAGGAGTTGGTCTTGGTCTTCTGGCTGATGTTCTGTTATCTTAACATGAC	1680
Db	1710	CTATGTTATCTTAAGGAGTTGGTCTTGGTCTTCTGGCTGATGTTCTGTTATCTTAACATGAC	1769
Qy	1681	CACAGTTTGTAAAGTAC	1696
Db	1770	CACAGTTTGTAAAGTAC	1785
RESULT 3			
AK091952			
LOCUS	Homo sapiens	cdna FLJ34633	1785 bp
DEFINITION	Homo sapiens	clone KIDNE2015710.	linear
ACCESSION	AK091952		
VERSION	AK091952.1	GI-21750433	
KEYWORDS	oligo capping; f18 (full insert sequence).		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, K., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Iehibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotaka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,		

TITLE		Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs	
JOURNAL	Nat. Genet. 36 (1), 40-45 (2004)		
PUBMED	14702039		
REFERENCE	2		
AUTHORS	Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Watsutsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.		
TITLE		NEDO human cDNA sequencing project	
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1785)		
AUTHORS	Isogai, T. and Yamamoto, J.		
AUTHORS	Direct Submission		
JOURNAL	Submitted (04-JUN-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisearazu, Chiba 292-0812, Japan		
COMMENT		(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.	
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CDS			
ORIGIN			
Query Match	98.8%;	Score 1692.8;	DB 8; Length 1785;
Best Local Similarity	99.9%;	Pred. No. 0;	
Matches 1694;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
Qy	1	ATGCGCCCGCTGGACACCCCGCCAGCATCTGGCGCTCCACCGCTTGGGACCGTGGGAG	60
Db	90	ATGCGCCCGCTGGACACCCCGCCAGCATCTGGCGCTCCACCGCTTGGGACCGTGGGAG	149
Qy	61	CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACTCAGCCCCCACCACGCGC	120
Db	150	CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACTCAGCCCCCACCACGCGC	209
Qy	121	CGCACCCGTAGACGACCCCAAGACCCCTGGCCACCATGGGCCAGAGACATTACCTTC	180
Db	210	CGCACCCGTAGACGACCCCAAGACCCCTGGCCACCATGGGCCAGAGACATTACCTTC	269

Db	1350	GGACGAGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCTTCTGGCTCTCTCC	1409
Qy	1321	TGCTTGGCTGACTGGGTTCTCTGACCATGTCATTTTCACTGGGCCCATGGGATCTACATC	1380
Db	1410	TGCTTGGCTGACTGGGTTCTCTGACCATGTCATTTTCACTGGGCCCATGGGATCTACATC	1469
Qy	1381	TCCTTGATCCCATGCTGGTCTGATCCCTGCGAGGGCCCTTCTTCTGCTCTCATGTGCT	1440
Db	1470	TCCTTGATCCCATGCTGGTCTGATCCCTGCGAGGGCCCTTCTTCTGCTCTCATGTGCT	1529
Qy	1441	TCAGTGGCTGATCATGGAAGTAAGAGTTAGGCAATTAACCTTCTGGGAGTGAACCTTG	1500
Db	1530	TCAGTGGCTGATCATGGAAGTAAGAGTTAGGCAATTAACCTTCTGGGAGTGAACCTTG	1589
Qy	1501	ACTCCATCCCTTATTCGCCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT	1560
Db	1590	ACTCCATCCCTTATTCGCCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT	1649
Qy	1561	TCAACAGTTAAAGAGCTTATCTTAAATGATTTATTTGTTATTTGGGGTGGGAGGCCCACT	1620
Db	1650	TCAACAGTTAAAGAGCTTATCTTAAATGATTTATTTGTTATTTGGGGTGGGAGGCCCACT	1709
Qy	1621	CTATGTTATCTTAAGGAGTTGGTCTTGGTCTTGGCTGATGTTCTGTATCTTAACATGAC	1680
Db	1710	CTATGTTATCTTAAGGAGTTGGTCTTGGTCTTGGCTGATGTTCTGTATCTTAACATGAC	1769
Qy	1681	CACAGTTTGAAGTAC	1696
Db	1770	CACAGTTTGAAGTAC	1785
RESULT 4			
BC033143			
LOCUS			
DEFINITION	Homo sapiens chromosome 1 open reading frame 172, mRNA (cdna clone		
ACCESSION	MGC:45763 IMAGE:3960220), complete cds.		
VERSION	BC033143		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1679)		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvachenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.		
CONSTRM	Mammalian Gene Collection Program Team		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1679)		
AUTHORS	NIH MGC Project		
CONSTRM	Direct Submission		
TITLE			

JOURNAL	Submitted (25-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgabs-x@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Mokea, Johnson Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR Santos, Duane Smalus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Aaim Siddiqui, Steven Jones, Rob Holt, Marco Marra.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 43 Row: c Column: 17.		
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CDS			
ORIGIN	Query Match 94.6%; Score 1620.2; DB 8; Length 1679; Best Local Similarity 99.8%; Pred. No. 0; Matches 1622; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
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Qy	137	ACCCCAAGACCTTGGCCACCATGGGCCAGAGAGCATTTACCTTCATCTCTGGCTCTGCTG	196
Db	61	ACCCCAAGACCTTGGCCACCATGGGCCAGAGAGCATTTACCTTCATCTCTGGCTCTGCTG	120
Qy	197	AGCCGGCCCTTCTAGTCTCCCACTGCTGCTCTGGGACCCCTGGGTGTGGAGTGGT	256
Db	121	AGCCGGCCCTTCTAGTCTCCCACTGCTGCTCTGGGACCCCTGGGTGTGGAGTGGT	180
Qy	257	GCCTGGCTGCTTCTGCTTCCCGCGCTGCGGGATTCCTCCAGCGCTGTGGAGCTGTG	316
Db	181	GCCTGGCTGCTTCTGCTTCCCGCGCTGCGGGATTCCTCCAGCGCTGTGGAGCTGTG	240
Qy	317	TGCGGGGATGACAGCCCTCTGCTGTCTACTGAGGACCTCCACTGAGGGGACTGTGGAAGCCA	376

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QY 977 CAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTGGGCTCAGCTCAGCCAGC 1036
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QY 1037 ATGAGCTGACGATGACGATCTCCAGGAGACGACTGCAGATGCCATCGCCCGGAAGCTGA 1096
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DEFINITION Sequence 56 from Patent WO02068633.
ACCESSION AX535029
VERSION AX535029.1 GI:25261664
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1
Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
Compositions and methods relating to lung specific genes and
proteins
Patent: WO 02068633-A 56 06-SEP-2002;
Diadexus, Inc. (US)
Location/Qualifiers
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Best Local Similarity 99.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;

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RESULT 6
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LOCUS AX535090
DEFINITION Sequence 117 from Patent WO02068633.
ACCESSION AX535090
VERSION AX535090.1 GI:25261789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Macina,R.A., Recipon,H., Chen,S.Y., Sun,Y., and Liu,C.
TITLE Compositions and methods relating to lung specific genes and proteins
JOURNAL Patent: WO 02068633-A 117 06-SEP-2002;
Diadexus, Inc. (US)
FEATURES
source 1. .1977
Location/Qualifiers
/organism="Homo sapiens"
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ORIGIN
Query Match 93.5%; Score 1602.4; DB 6; Length 1977;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;

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RESULT 7
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DEFINITION Sequence 3609 from Patent WO02068579.
ACCESSION CQ717675
VERSION CQ717675.1 GI:42278532
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 3609 06-SEP-2002;
PE Corporation (NY) (US)
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Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
DEFINITION
Human DNA sequence from clone RP11-344H11 on chromosome 1. Contains
the NR0B2 gene for nuclear receptor subfamily 0 (group B, member
2), the 5' end of a novel gene (FLJ12455), the NUDC gene for nuclear
distribution gene C homolog (A. nidulans), a novel gene (FLJ34633),
a ribosomal protein l12 (RP112) pseudogene, a ribosomal protein l32
(RP132) pseudogene, a novel pseudogene (DC2), two novel genes and
two CpG islands, complete sequence.
ACCESSION
AL356390
VERSION
AL356390.24 GI:21436506
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KEYWORDS
SOURCE
ORGANISM

HTG; DC2; FLJ12455; FLJ34633; NR0B2; NUDC; RP112; RPL32.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 140207)

REFERENCE
AUTHORS
TITLE
JOURNAL

Glithero, R.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk

COMMENT

On Jun 17, 2002 this sequence version replaced gi:20218554.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP11-344H11 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.

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DEFINITION
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VERSION AL592304.1 GI:114586390
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
McLay, K.
Direct Submission
Submitted (24-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
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ORIGIN

Query Match 60.5%; Score 1035.8; DB 14; Length 111738;
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Matches 1037; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Center project name: dJ426N7
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Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 110287 bases at least Q40
Consensus quality: 110500 bases at least Q30
Consensus quality: 110681 bases at least Q20
Insert size: 111138; sum-of-contigs
Quality coverage: 11.23x in Q20 bases; sum-of-contigs Quality
coverage: 10.67x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 18159 35144: contig of 16986 bp in length
* 35145 35244: gap of 100 bp
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MGC.				
Mus musculus (house mouse)				
Mus musculus				
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Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
12477932				
2 (bases 1 to 1680)				
Strausberg, R.				
Direct Submission				
Submitted (27-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
NIH-MGC Project URL: http://mgc.nci.nih.gov				
Contact: MGC help desk				
Email: cgabs-r@mail.nih.gov				
Tissue Procurement: Jeffrey Green M.D.				
cDNA Library Preparation: Life Technologies, Inc.				
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center				
Center code: BCM-HGSC				
Web site: http://www.hgsc.bcm.tmc.edu/cdna/				
Contact: amg@bcm.tmc.edu				
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.				
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov				
Series: IRAK plate: 16 Row: p Column: 2				
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19526881.				
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ORIGIN
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DB 1188 TTCCAGGCGACCCAGACAGACTTCTTCCAGGCGACCTTGTCTCAGGCTGATGATGATGCC 1247
QY 1201 CTGCCAGGCGGAGCTGCCACACCTTCTGGGAGAGCATGGCTTACAGAAATGAGAGGG 1260
DB 1248 CTACTGCGCCAGCAGTACGCGCTCTCTGGAAGAGCATAGCCAGC---GGAGGAGAG 1303
QY 1261 GGACGAGGACCC---CTGTGGGAGAGGCTTAGACCTGAGCAGTGGCCACTCTGCGCTCC 1317
DB 1304 GAACGAGGACCTTGTGTGGGCGGCTCTGAGCCCGAGAGCAGTGAACCTCTCTGCGCTTC 1363
QY 1318 TCTGCTGCTGGCTGACTGGGCTTCTGACCATGCTGCAATTTTCACTGGGCGCATGGATCTAC 1377
DB 1364 TGCTTTTGTGATCC-----CCTTAGACACATACATTTTACAGGGCCATGTCGCCAT 1418
QY 1378 ATCTCTTGCATCCCGAGCTGTGCTGATCCCTGCGAGGGCCCTTC 1423
DB 1419 ACCCCCTT-----CCAGCTGGCTGACTGCTGGCTGGGCTCTCTC 1458
```

RESULT 11

BC079148
LOCUS
DEFINITION
Rattus norvegicus similar to hypothetical protein FLJ34633, mRNA
(CDNA clone MGC:94165 IMAGE:7128510), complete cds.

BC079148
VERSION
BC079148.1 GI:50927712

KEYWORDS
MGC.

SOURCE
Rattus norvegicus (Norway rat)

ORGANISM
Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE
1 (bases 1 to 1718)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,


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Db 104729 AGCATCACGAGGACTACCACTGGATGAGCAAGACGCCGAGGCGCCTGGTGCGGGGC 104788
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QY 901 ATCATTCGATAGTATCCGGAAGACCGCTGCTGCGGCCACAGACCTCGGAGGGTCTGTCA 960
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RESULT 13
AC095979
LOCUS
DEFINITION
Rattus norvegicus clone CH230-11020, WORKING DRAFT SEQUENCE, 3
unordered pieces.
AC095979
VERSION
GI:24818145
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
REFERENCE
Muzny, D., Marie, M., Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J.,
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Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Prannkoeb, C.,
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Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
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Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
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Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,
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Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P.,
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Yu, E., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 235419)
Worley, K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235419)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:22772470.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project information
Center project name: GEBU
Center clone name: CH230-11020
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 225536 bases at least Q40
Consensus quality: 227458 bases at least Q30
Consensus quality: 228649 bases at least Q20
Estimated insert size: 235033; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 221492: contig of 221492 bp in length
* 221493 221592: gap of unknown length
* 221593 228651: contig of 7059 bp in length
* 228652 228751: gap of unknown length
* 228752 235419: contig of 6668 bp in length.
* Location/Qualifiers
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/clone="CH230-11020"
2958. .3864
/note="clone boundary
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83146 AGCCCAACAGATTATGCTCTGGAACGAATGATGAGCGCTCCAGCCCCCACCAGGCGGT 83205
121 CGCACCGGTAGACAGACCCCAAGACCTTGGCCACCATGGGCCAGAGCATTTACCTTC 180
83206 CGCACCGGAGGCGACACCTTAAGGACCTTGGCCACCATGGGCCAGAGCATTTACCTTC 83265
181 ATCTCTGGCTCTGTCAGCGCGGCTTGTAGTCTCCCACTGCTGCTCTGCTCTGCGGACCC 240
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361 GCGACTGCTGAAGCCTGAGCGGATGCGGACCAAGGACCAATGGAGTGCGCCCGGCTGATCGT 420
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421 GCACCCCGGATGAGCGGATGCGGACCAAGGACCAATGGAGTGCGCCCGGCTGATCGT 480
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601 AGCTGTGCGGACTCTGCTGCAAGGACCAAGGACCAATGGAGTGCGCCCGGCTGATCGT 660
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781 AAGTGACATCAGACACTGTGTTCTTGGAGAACCAAGGACCAATGGAGTGCGCCCGGCTGATCGT 840
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Query Match 45.1%; Score 773.4; DB 14; Length 235419;
Best Local Similarity 84.7%; Pred. No. 2.2e-178;
Matches 880; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

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83926 AGCATCACGCGGACTACCACTGGATGACGAGGATGCTGAGGGCGGCTGTAGTGGCG 83985
901 ATCATTCGATAGTACCGGAAAGAGCGGCTGCTGCGCCACAGACCTCGGAGGGTCTGTTCA 960
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961 ACTCGGGCTGCTGCGCCAAACCGCTGCTGCGCCCTGACAGTGGCCATGAGACCATGTGGG 1020
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84103 TCTGGCTCAGCCAGGATG 84121

AC118963 249406 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-180E4, WORKING DRAFT SEQUENCE.
AC118963
HTG: HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus;
1 (bases 1 to 249406)
Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleaveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
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RESULT 14
AC118963/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
 Direct Submission
 2 (bases 1 to 249406)

TITLE JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Nov 15, 2002 this sequence version replaced gi:23269749.
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GVHY

Center clone name: CH230-180E4

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 21337 bases at least Q40

Consensus quality: 215358 bases at least Q30

Consensus quality: 217213 bases at least Q20

Estimated insert size: 223109; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 249406: contig of 249406 bp in length.

FEATURES

source

1. .249406

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-180E4"

/note="wgs_contig"

ORIGIN

Query Match

Best Local Similarity 45.1%; Score 773.4; DB 14; Length 249406;

84.7%; Pred. No. 2.2e-178;

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QY	61	CGGCCAACAGAGCTATGCTGGAGACATATGATAAACCACTTCAGCCCCCACCACAGCCGC	120							
Db	14696	AGGCCACACAGAGTTATGCTGGAAAGAAATGATAGCGCTCCACGCCCCACACAGGCCGT	14637							
QY	121	CGACCCGTAGACACAGACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCATTACCTTC	180							
Db	14636	CGACCCGCGAGGCCAGACCCCTAAGGACCTTGGCCACCATGGGCCAGAGAGCATTACCTTC	14577							
QY	181	ATCTCTGGCTCTGCTGAGCGGCGCTTGGAGTCCCGCCCTTGGCTGCTGCTGGGCGACC	240							
Db	14576	ATTTCAGGCTCTGCAGAACACGACCAAGAGCCCCCAACTGCTGCTCTCTGGGCGCCC	14517							
QY	241	TGGGTGTGGGAGTGGTGGCGGCTGCTTCTGCTTCCGCGCTGCGGGATTCCTCCAG	300							
Db	14516	TGGGCTTGGGACTGGTGTAGGGCTGCCCTTCTCGACGCTGCAGGGATTCCTCCAG	14457							
QY	301	CGCTGTGAGCCTGTGTGCGGGGATGAGCCCTTGCCTGCTCTACTGAGACTCCACTGAG	360							
Db	14456	CGCTGTGAGCCTGTGTGCGGAGCTGTAGCCCTGCTTATCTGTGGAGACCCCATTTGAA	14397							
QY	361	GGGACTGCTGAAGCCAACTGGGCCAAGGAGACAAATGAGTGCCTCCCGCCAGCCCTGATCT	420							
Db	14396	GGGTCTTGGAAAGCCGCTTGGGCCAAGGAAACAAGGTGTGCTTCCAGCCAGACCA	14337							
QY	421	GCACCCCGCCAGCCGCGGAGTGGCCAGCGGCTCAAGTCAACCATGGGACGAGCTTCAGC	480							
Db	14336	GCACCCCGCCAGCCGCGGAGTGGCCAAAGCTCAAGACCAAGCATGGGACGAGCTTCAGC	14277							
QY	481	TACCCCGATTTAAGCTCAAGGATTCCTGTGTATTCCTACCGAGGGCCACCTCCCA	540							
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QY	781	AAGTGACATCAGACATGTGTTCTTGGAGAGAACAGTAAGATCTGGACCTTATCAGC	840							
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RESULT 15
AC126312/c
LOCUS
DEFINITION
AC126312
AC126312.4 GI:24941465
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus;
1 (bases 1 to 256017)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amarantunga, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
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DeLaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
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Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, D.C., Lewis, L.,
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Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
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Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savary, G.,
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Sodergren, E., Sonaika, T., Sparks, A., Stanley, H., Stone, H.,
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Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 256017)
Worley, K.C.
Direct Submission
TITLE
SUBMITTED (05-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 256017)
Worley, K.C.
Direct Submission
TITLE
SUBMITTED (13-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23267435.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: TUNJ
Center clone name: CH230-1B9
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 214827 bases at least Q40
Consensus quality: 219116 bases at least Q30
Consensus quality: 221911 bases at least Q20
Estimated insert size: 222841; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 83721: contig of 83721 bp in length
* 83722 83821: gap of unknown length
* 83822 253567: contig of 169746 bp in length
* 253568 253667: gap of unknown length
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FEATURES
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/note="wgs contig"
219978..221353
/note="wgs contig"
253568..253667
/estimated_length=unknown

ORIGIN
Query Match 45.1%; Score 773.4; DB 14; Length 256017;
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Matches 880; Conservative 0; Mismatches 156; Indels 3; Gaps 1;
1 ATGCCCGCCCTGGACACACCCGCCGCTCCACGTTGGGACCGTGGAG 60

Job time : 8485 secs

Db	155744	ATGCCACAGCCGGGACACGCCCGCCCATCGTCTGGGCTCCACGCTTGGGCGCCCTGGGAG	155685
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Db	155504	TGGGGTTGGGACTGGTGTAGGGCTGCCCTTCTGCTTCCAGCGCTGACGGATTCCTCCAG	155445
Qy	301	CGCTGTGGAGCCTGTGTGCGGGGATGACGCCCTTGCCTGTCTACTAGGACTTCCACTGAG	360
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Db	155264	TACCTGATGTTAAGCTCAAGGGCATCCCGGTCTACCCCTACCGCATGCCACCTCCCCC	155205
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Db	155204	GTCCCTGACCGCGSACTCCTGCTGCAAGGAGCCCTTGGCAGACCCCTCTCCACACCGCAC	155145
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Db	155024	GTGCTTATTTTCAAGAAGCTGACAGAGCTGTTCAGTGTACATCAGATTGACGAGCTGGCC	154965
Qy	781	AAGTGCACATCAGACACTGTGTTCTCTGGAGAAGACCACTAAGATCTCGGACCTTATCAGC	840
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Qy	841	AGCATCAAGCAGGACTACCACTGGATGACGAGGATCTGAGGGCCGCTGTGATCGCGCG	900
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Db	154784	GCCGCTCTACTGCTC---CTGCTGCTGCCCCGACAGTGGCCATGAGACCATGTGGGC	154728
Qy	1021	TCAGGCTTCAGCCAGGATG	1039
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 19:35:11 ; Search time 1063 Seconds
(without alignments)
10739.999 Million cell updates/sec

Title: US-09-989-890-105

Perfect score: 1713

Sequence: 1 atgcccgcctggacacc.....tactcggccgcgaccacgc 1713

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	100.0	1713	8	ABT13390 Breast sp
2	1694.6	98.9	2392	10	ADD01260 Human nuc
3	1692.8	98.8	1785	10	ADB62645 Human cDN
4	1602.4	93.5	1977	6	ABX92075 Lung spec
5	1602.4	93.5	1977	6	ABX92014 Lung spec
6	763	44.5	791	14	AEAL19545 Novel hum
7	607.6	35.5	654	6	ABT07645 Human bre
8	463.2	27.0	728	2	AAZ17414 Human gen
9	385	22.5	385	6	ABX92013 Lung spec
10	380.2	22.2	386	6	ABT07644 Human bre
11	380.2	22.2	386	8	ABT13389 Breast sp
12	352.6	20.6	393	5	AAF64421 Novel hum
13	347	20.3	427	5	AAF66376 Novel hum
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	25	43.6	2.5	346	3	AAA34171		Aaa34171 Human ade
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	29	43.6	2.5	7033	3	AAF20844		Aaf20844 Human low
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C	37	43	2.5	1908	13	ADR89879		Adr89879 Polynucle
C	38	43	2.5	2289	9	ACC59893		Acc59893 Human REM
C	39	43	2.5	2359	4	AAS28798		Aas28798 Human imm
C	40	43	2.5	2359	10	ADB31523		Adb31523 Human cDN
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ALIGNMENTS

RESULT 1

ABT13390
ID ABT13390 standard; DNA; 1713 BP.

AC ABT13390;

DT 30-JAN-2003 (first entry)

DE Breast specific related polynucleotide SEQ ID NO 105.

KW Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer;
KW metastatic; breast cancer; breast specific; human; db.

OS Homo sapiens.

PN WO200277232-A2.

PD 03-OCT-2002.

PF 21-NOV-2001; 2001WO-US043815.

PR 22-NOV-2000; 2000US-0252509P.

PA (DIAD-) DIADEXUS INC.

PI Salceda S, Macina RA, Recipon H, Pluta J, Sun Y, Liu C;

DR WPI; 2003-018927/01.

PT New isolated nucleic acid molecule, useful for treating breast cancer,
PT in a patient.

PS Claim 1; Page 250-251; 377pp; English.

CC The invention relates to a novel isolated nucleic acid molecule
CC comprising: a sequence encoding a sequence comprising 11-1518 amino acids
CC ; a sequence comprising 190-8144 bp; or a sequence that selectively
CC hybridizes to, or having at least 60% identity with the 11-1518 amino
CC acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are
CC useful for treating breast cancer, and diagnosing or monitoring the
CC presence of metastases of breast cancer in a patient. The polynucleotides

CC of the invention can be used to treat disorders by gene therapy. This
CC polynucleotide represents a breast specific related sequence of the
CC invention

XX	SQ	Sequence	1713 BP; 344 A; 553 C; 468 G; 348 T; 0 U; 0 Other;	
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		Best Local Similarity	100.0%; Pred. No. 0;	
		Matches 1713; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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QY	61	CGGCCAACAGAGCTATGCTCGAGACATATGATAAACCACTCAGCCCCCCACCAAGCCGC	120	
DB	61	CGGCCAACAGAGCTATGCTCGAGACATATGATAAACCACTCAGCCCCCCACCAAGCCGC	120	
QY	121	CGCACCCGTAGACACACCCCAAGGACCTTGGCCACCATGGGCCAGAGACATTAACCTTC	180	
DB	121	CGCACCCGTAGACACACCCCAAGGACCTTGGCCACCATGGGCCAGAGACATTAACCTTC	180	
QY	181	ATCTCTGGCTCTGCTGAGCGCGCCCTTGAGTCCCCACCTGCTGCTCTGGCGAACCC	240	
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QY	241	TGGGTGTGGAGTGTGCGGGGTGCTTCTGCTTCCGGCGCTGCGGGATTCCTCCAG	300	
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QY	301	CGCTGTGGAGCTGTCTGCGGGATGACGCCCTGCTGCTACTGAGACTCCACTGAG	360	
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QY	541	GCCCTGTATCGGACTCCTGCTGCAAGGAGCCACTGGCCGATCCCCACCCCATGCGACAC	600	
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QY	601	AGCCTGCCAGACACTTTGGCAGTAGTCTCTGCTGGCTCCGAGGACTACTATTCTTTCCAT	660	
DB	601	AGCCTGCCAGACACTTTGGCAGTAGTCTCTGCTGGCTCCGAGGACTACTATTCTTTCCAT	660	
QY	661	GAGTCGAGCTGACCTGCGGAGATGGGCGAGTGGCTCCATGTCGAGCGAGAGAAATGAT	720	
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QY	901	ATCATTTGCAATTAGTACCCGAAAGACCGGTGCTCGGCCACAGACCTCGGAGGGTCGTTCA	960	
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QY	1021	TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGATGAGATGCC	1080	
DB	1021	TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGATGAGATGCC	1080	
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DB	1201	CTGCCAGGCCAGCTGCCACACCTTTCTGGAGAGCATGCGCTACAGATGAAGAGGG	1260	
QY	1261	GGACCAAGAACCCCTGTGGGAGAGGCTTAGACTGAGCAGTGGCCACTCTGGCTCCTCC	1320	
DB	1261	GGACCAAGAACCCCTGTGGGAGAGGCTTAGACTGAGCAGTGGCCACTCTGGCTCCTCC	1320	
QY	1321	TGCTTGGCTGACTGGGTTCTTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC	1380	
DB	1321	TGCTTGGCTGACTGGGTTCTTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC	1380	
QY	1381	TCCTTGCACTCCCGAGCTGTGATCCCTGCGAGGCCCTTCTCTTCTGCTCATGGTCT	1440	
DB	1381	TCCTTGCACTCCCGAGCTGTGATCCCTGCGAGGCCCTTCTCTTCTGCTCATGGTCT	1440	
QY	1441	TCAGTGGCTCATCATGGAAGTAAAGGATTTAGGCATTTACCTTCTGGAGTGAACCCCTG	1500	
DB	1441	TCAGTGGCTCATCATGGAAGTAAAGGATTTAGGCATTTACCTTCTGGAGTGAACCCCTG	1500	
QY	1501	ACTCCATCCCTTATTCGCCACCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT	1560	
DB	1501	ACTCCATCCCTTATTCGCCACCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT	1560	
QY	1561	TCACAGTTTAAAGAGCTTATCTTAAATGTATTTATTTGGGGGTGGCGAGGCCCACT	1620	
DB	1561	TCACAGTTTAAAGAGCTTATCTTAAATGTATTTATTTGGGGGTGGCGAGGCCCACT	1620	
QY	1621	CTATGTTATTTAAGAGTGGTCTGGTCTTGGCTGATGTTCTGTATCTTAACATGAC	1680	
DB	1621	CTATGTTATTTAAGAGTGGTCTGGTCTTGGCTGATGTTCTGTATCTTAACATGAC	1680	
QY	1681	CACAGTTTGTAAAGTACTCCGCGCGGACCAACGC	1713	
DB	1681	CACAGTTTGTAAAGTACTCCGCGCGGACCAACGC	1713	

RESULT 2

ADD01260

ID ADD01260 standard; cDNA; 2392 BP.

XX AC ADD01260;

XX AC AC

DT 01-JAN-2004 (first entry)

XX

DE Human nucleic acid-associated protein NAAP-41 cDNA SEQ ID NO:98.

XX

XX

KW human; nucleic acid-associated protein; NAAP; cytostatic;

KW antiarteriosclerotic; anti-HIV; antiallergic; cerebroprotective;

KW antiparkinsonian; anticonvulsant; nootropic; neuroprotective;

KW antiinflammatory; ophthalmological; thyromimetic; antiarthritic;

KW hepatotropic; antibacterial; virucide; protozoacide; antiparasitic;

KW fungicide; gene therapy; cell proliferative disease; cancer;

KW atherosclerosis; hepatitis; neurological disorder; Parkinson's disease;

KW Alzheimer's disease; stroke; epilepsy; developmental disorder;

KW renal tubular acidosis; anaemia; glaucoma; hypothyroidism;

KW autoimmune disorder; inflammatory disorder; AIDS; allergy;
KW atopic dermatitis; arthritis; infection; gene; ss.
XX Homo sapiens.
XX WO2003054219-A2.
XX 03-JUL-2003.
XX 18-DEC-2002; 2002WO-US041115.
XX 19-DEC-2001; 2001US-0343004P.
XX 11-JAN-2002; 2002US-0347633P.
XX 25-JAN-2002; 2002US-0351749P.
XX 22-FEB-2002; 2002US-0359498P.
XX (INCY-) INCYTE GENOMICS INC.
XX Azimzai Y, Baughn MR, Becha SD, Borowsky ML, Burford N;
PI Elliott VS, Emerling BM, Forsythe IJ, Gorvad AE, Griffin JA;
PI Kable AE, Khare R, Lal PG, Lee EA, Lee SY, Li JX, Marquis JP;
PI Ramkumar J, Richardson TW, Sprague WW, Swarnakar A, Tang YT;
PI Chawla NK, Warren BA, Yue H;
XX WPI; 2003-559157/52.
DR P-PSDB; ADD01203.
XX
XX New human nucleic acid-associated proteins (NAAP), useful for diagnosing,
PT treating and preventing diseases or conditions associated with the
PT aberrant NAAP expression, e.g. cancer, hepatitis, AIDS, atherosclerosis,
PT infections.
XX
XX Claim 5; SEQ ID NO 98; 405pp; English.
XX
XX The present invention describes human nucleic acid-associated proteins
CC designated NAAP-1 to NAAP-57. The human NAAPs have cytostatic,
CC antiarteriosclerotic, anti-HIV, antiallergic, cerebroprotective,
CC antiparkinsonian, anticonvulsant, neurotropic, neuroprotective,
CC antiinflammatory, ophthalmological, thymomimetic, antiarthritic,
CC hepatotropic, antibacterial, virucide, protozoacide, antiparasitic and
CC fungicide activities, and can be used in gene therapy. The NAAP protein
CC and polynucleotide sequences can be used in diagnosing, treating and
CC preventing diseases or conditions associated with the decreased
CC expression or overexpression of NAAP, such as cell proliferative diseases
CC (e.g. cancer, atherosclerosis, hepatitis), neurological disorders
CC (Parkinson's disease, Alzheimer's disease, stroke, epilepsy),
CC developmental disorders (renal tubular acidosis, anaemia, glaucoma,
CC hypothyroidism), autoimmune/inflammatory disorders (AIDS, allergies,
CC atopic dermatitis, arthritis) and infections (e.g. bacterial, viral,
CC parasitic, protozoal, fungal). The present sequence encodes human NAAP-
CC 41, from the present invention.
XX
XX Sequence 2392 BP; 471 A; 743 C; 674 G; 504 T; 0 U; 0 Other;
Query Match 98.9%; Score 1694.6; DB 10; Length 2392;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1697; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ATGCGCGCGCTGAGACACCGCCCGGAGCATCTGGGCTCCAGCTTGGACCGTGGAG 60
DB 255 ATGCGCGCGCTGAGACACCGCCCGGAGCATCTGGGCTCCAGCTTGGACCGTGGAG 314
QY 61 CGGCCAACAGAGCATGTCTGGAGACATATGATAAACCACTCAGCGCCCAACCAAGCCGC 120
DB 315 CGGCCAACAGAGCATGTCTGGAGACATATGATAAACCACTCAGCGCCCAACCAAGCCGC 374
QY 121 CGCACCGGTAGACAGACACCGCCAGGACCTGGCCACCATGGGCGAGAGCATTAACCTTC 180
DB 375 CGCACCGGTAGACAGACACCGCCAGGACCTGGCCACCATGGGCGAGAGCATTAACCTTC 434
QY 181 ATCTCTGGCTCTGCTGAGCGCGCGCTTGTAGTCCCGCCACCTGCTGCTGCGGACCC 240
DB 435 ATCTCTGGCTCTGCTGAGCGCGCGCTTGTAGTCCCGCCACCTGCTGCTGCGGACCC 494

QY 241 TGGGTGTGGAGTGTGTGCGGGGTGCGGCTTGTCTTGTCTTGTCTGCGCGCTGCGGGATTCCTCCAG 300
DB 495 TGGGTGTGGAGTGTGTGCGGGGTGCGGCTTGTCTTGTCTTGTCTGCGCGCTGCGGGATTCCTCCAG 554
QY 301 CGCTGTGGAGCTGTGTGCGGGGTGCGGCTTGTCTTGTCTTGTCTGCGCGCTGCGGGATTCCTCCAG 360
DB 555 CGCTGTGGAGCTGTGTGCGGGGTGCGGCTTGTCTTGTCTTGTCTGCGCGCTGCGGGATTCCTCCAG 614
QY 361 GGGACTGTCTGAAGCAACCTGGGCAAGGAGCAACAATGGAGTGGCGCCCGCCAGCCCTGATCGT 420
DB 615 GGGACTGTCTGAAGCAACCTGGGCAAGGAGCAACAATGGAGTGGCGCCCGCCAGCCCTGATCGT 674
QY 421 GCAACCCCGCAGCGCGGGGATGGCGCGGCTCAAGTCAACCAATGGGCGAGGATTCAGC 480
DB 675 GCAACCCCGCAGCGCGGGGATGGCGCGGCTCAAGTCAACCAATGGGCGAGGATTCAGC 734
QY 481 TACCCCGATGTTAAGCTCAAAAGGCATCCCTGTGTATCCCTACCGAGGGGACCTCCCTCCA 540
DB 735 TACCCCGATGTTAAGCTCAAAAGGCATCCCTGTGTATCCCTACCGAGGGGACCTCCCTCCA 794
QY 541 GCCCTGTGATGCGGACTCTCTGCTGCAAGGAGCCACTGGCCGATCCCGCCATTCGACAC 600
DB 795 GCCCTGTGATGCGGACTCTCTGCTGCAAGGAGCCACTGGCCGATCCCGCCATTCGACAC 854
QY 601 AGCTGCGCCAGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 855 AGCTGCGCCAGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
QY 661 GAGTGGAGCTGCACTGCGGAGATGGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 915 GAGTGGAGCTGCACTGCGGAGATGGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 974
QY 721 GTCTCATCTTCAAGAGCTGACAGAGCTGCTTCAAGGCTACACAGATTCAGATGAGCTGGCC 780
DB 975 GTCTCATCTTCAAGAGCTGACAGAGCTGCTTCAAGGCTACACAGATTCAGATGAGCTGGCC 1034
QY 781 AAGTGCATCATGACACCTGTGTTCTTGGAGAACACAGTAAAGATTCGGACCTTATCAGC 840
DB 1035 AAGTGCATCATGACACCTGTGTTCTTGGAGAACACAGTAAAGATTCGGACCTTATCAGC 1094
QY 841 AGCATCACCGAGACTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 1095 AGCATCACCGAGACTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1154
QY 901 ATCATTTGCAATAGTACCCGAAAGAGCGTGTCTGCGCCACAGACCTCGGAGGGTCTGTCA 960
DB 1155 ATCATTTGCAATAGTACCCGAAAGAGCGTGTCTGCGCCACAGACCTCGGAGGGTCTGTCA 1214
QY 961 ACTCGGGCTGCTGCGCCCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 1215 ACTCGGGCTGCTGCGCCCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1274
QY 1021 TCAGGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGGACGATGAGATGAGCTGCGC 1080
DB 1275 TCAGGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGGACGATGAGATGAGCTGCGC 1334
QY 1081 ATCGCCCGGAAGCTGAGGGCTTATGAGCTTCCAGGGTACCCAGAGCCATGATCTATCC 1140
DB 1335 ATCGCCCGGAAGCTGAGGGCTTATGAGCTTCCAGGGTACCCAGAGCCATGATCTATCC 1394
QY 1141 TTCAGGGCAACGACACAGATCTGCTGCGGGGCAACCTTGTCTCAGGTTGATCTGCTAAACC 1200
DB 1395 TTCAGGGCAACGACACAGATCTGCTGCGGGGCAACCTTGTCTCAGGTTGATCTGCTAAACC 1454
QY 1201 CTGCGAGGCGGAGCTGCGCACACCTTCTGGGAGAGCATGGGCTACAGATGAGAGGG 1260
DB 1455 CTGCGAGGCGGAGCTGCGCACACCTTCTGGGAGAGCATGGGCTACAGATGAGAGGG 1514
QY 1261 GGACACGAGAACCCCTGCTGGGAGAGGCTTAGACCTGAAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1515 GGACACGAGAACCCCTGCTGGGAGAGGCTTAGACCTGAAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCT 1574

QY 601 AGCTGCCAGCAGCTTTGGCAGTAGTCTCTGGTCCGAGGAGTACTATTTCTTTCCAT 660
Db 690 AGCTGCCAGCAGCTTTGGCAGTAGTCTCTGGTCCGAGGAGTACTATTTCTTTCCAT 749
QY 661 GAGTCGAGCTGACCTTGGCGAGATGGGAGTGGTCTCCATGTCGAGCCGAGAAATTTGAT 720
Db 750 GAGTCGAGCTGACCTTGGCGAGATGGGAGTGGTCTCCATGTCGAGCCGAGAAATTTGAT 809
QY 721 GTCTCATCTTTCAAGAGCTGACAGAGCTTTTCAAGGCTACACAGATCGATGAGCTGGCC 780
Db 810 GTCTCATCTTTCAAGAGCTGACAGAGCTTTTCAAGGCTACACAGATCGATGAGCTGGCC 869
QY 781 AAGTCGACATCAGACATGTTCTTGGAGAGACAGGATGATGAGTCTCGGACCTTATCAGC 840
Db 870 AAGTCGACATCAGACATGTTCTTGGAGAGACAGGATGATGAGTCTCGGACCTTATCAGC 929
QY 841 AGCATCAGCAGGACTACCACTGGATGAGCAGATGCTGAGGGCGGCTGTGTCAGCGGC 900
Db 930 AGCATCAGCAGGACTACCACTGGATGAGCAGATGCTGAGGGCGGCTGTGTCAGCGGC 989
QY 901 ATCATTTGCAATTAGTACCCGAAAGAGCGTGTCTGCCCAACAGACCTCGAGGGTCTGTCA 960
Db 990 ATCATTTGCAATTAGTACCCGAAAGAGCGTGTCTGCCCAACAGACCTCGAGGGTCTGTCA 1049
QY 961 ACTCGGGCTGCTCCCNACCGCTGTGCCCTGACAGTGGCCATGAGACCATGTTGGC 1020
Db 1050 ACTCGGGCTGCTCCCNACCGCTGTGCCCTGACAGTGGCCATGAGACCATGTTGGC 1109
QY 1021 TCAGGTCTCAGCCAGGATGAGTGCAGATGTCAGATCTCCAGGAGACGACTGCAGATGCC 1080
Db 1110 TCAGGTCTCAGCCAGGATGAGTGCAGATGTCAGATCTCCAGGAGACGACTGCAGATGCC 1169
QY 1081 ATGCCCGGAGCTGAGGCTTTATGAGGTCTCAGGTTACCCAGAACCCATGATCTATCC 1140
Db 1170 ATGCCCGGAGCTGAGGCTTTATGAGGTCTCAGGTTACCCAGAACCCATGATCTATCC 1229
QY 1141 TTCAGGACACCGACACAGACTGTCGGGGGACCCCTTGTCTCAGGTGACTGCTAACCC 1200
Db 1230 TTCAGGACACCGACACAGACTGTCGGGGGACCCCTTGTCTCAGGTGACTGCTAACCC 1289
QY 1201 CTGCCAGGCCAGCTGCCACACCTTTCTGGAGAGAGCTGCGCTACAGATGAAAGGG 1260
Db 1290 CTGCCAGGCCAGCTGCCACACCTTTCTGGAGAGAGCTGCGCTACAGATGAAAGGG 1349
QY 1261 GGAACCAAGAACCCCTGTGGAGAGGCTTAGACCTGAAAGCAGTGCCTCTGCTCTCTCC 1320
Db 1350 GGAACCAAGAACCCCTGTGGAGAGGCTTAGACCTGAAAGCAGTGCCTCTGCTCTCTCC 1409
QY 1321 TGCCTTGGCTGACTGGGTTCTGGACCATGTGCAATTTCACTGGGCCATGGGATCTACATC 1380
Db 1410 TGCCTTGGCTGACTGGGTTCTGGACCATGTGCAATTTCACTGGGCCATGGGATCTACATC 1469
QY 1381 TCCTTGCATCCCGAGCTGGTCTGATCCCTGCCAGGGCCCTTCTCTCTGCTCATGCTCT 1440
Db 1470 TCCTTGCATCCCGAGCTGGTCTGATCCCTGCCAGGGCCCTTCTCTCTGCTCATGCTCT 1529
QY 1441 TCAGTGGGCTGATCATGGAAGTAAAGAGCTTAGGCAATTAACCTTCTGGAGTGAACCTTG 1500
Db 1530 TCAGTGGGCTGATCATGGAAGTAAAGAGCTTAGGCAATTAACCTTCTGGAGTGAACCTTG 1589
QY 1501 ACTCCATCCCTTATTTGCCACCCCTAAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAA 1560
Db 1590 ACTCCATCCCTTATTTGCCACCCCTAAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAA 1649
QY 1561 TCAACAGTTAAAGAGCTTATCTTAATGATGATTTGTTGGGGGTGGGAGGGCCCACT 1620
Db 1650 TCAACAGTTAAAGAGCTTATCTTAATGATGATTTGTTGGGGGTGGGAGGGCCCACT 1709
QY 1621 CTATGTTATGTTAAGAGTTGGTTCCTGGTTCCTGGTTCCTGATGTTCTGATCTTAAATGAC 1680
Db 1710 CTATGTTATGTTAAGAGTTGGTTCCTGGTTCCTGGTTCCTGATGTTCTGATCTTAAATGAC 1769
QY 1681 CACAGTTTGTAAAGTAC 1696

Db 1770 CACAGTTTGTAAAGTAC 1785

RESULT 4

ABX92075

ID ABX92075 standard; cDNA; 1977 BP.

XX AC ABX92075;

DT 08-MAY-2003 (first entry)

XX Lung specific nucleic acid (LSNA) #117.

XX Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
cancer monitoring; cancer staging; cancer imaging; lung cancer;
non-cancerous diseases of the lung; transgenic animal; gene; ss.

XX Homo sapiens.

XX WO200268633-A2.

XX 06-SEP-2002.

XX 21-NOV-2001; 2001WO-US043612.

XX 22-NOV-2000; 2000US-0252500P.

XX (DIAD-) DIADEXUS INC.

XX Macina RA, Recipon H, Chen S, Sun Y, Liu C;

XX WPI; 2002-713376/77.

XX New isolated human nucleic acid molecule and polypeptide, useful for
identifying, diagnosing, monitoring, staging, imaging and treating lung
cancer and non-cancerous diseases of the lung.

XX Claim 1; Page 266-267; 389pp; English.

XX The invention describes an isolated human nucleic acid (I) encoding any
of 120 10-1533 residue amino acid sequences (S1), given in the
specification, comprising any of 164 179-1241 base pair sequences (S2),
given in the specification. The methods and compositions of the present
invention are useful for identifying, diagnosing, monitoring, staging,
imaging and treating lung cancer and non-cancerous diseases of the lung.
They are also used for identifying lung tissue, monitoring and
identifying and/or designing antagonists of the polypeptide of the
invention, gene therapy, production of transgenic animals and production
of engineered lung tissue for treatment and research. This sequence
encodes a lung specific nucleic acid

XX Sequence 1977 BP; 393 A; 631 C; 554 G; 399 T; 0 U; 0 Other;

Query Match 93.5%; Score 1602.4; DB 6; Length 1977;

Best Local Similarity 99.0%; Pred. No. 0;

Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;

QY 1 ATGCCCGCCCTGGACACCCCGCCGAGCATCTGGGCTCCACGCTTGGACCGTGGAG 60

Db 254 ATGCCCGCCCTGGACACCCCGCCGAGCATCTGGGCTCCACGCTTGGACCGTGGAG 313

QY 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGCGC 120

Db 314 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGCGC 373

QY 121 CGCACCCGTAGACACCCCAAGGACCTTGGCCACCATGTGGGCCAGAGAGCATTTCTTC 180

Db 374 CGCACCCGTAGACACCCCAAGGACCTTGGCCACCATGTGGGCCAGAGAGCATTTCTTC 433

QY 181 ATCTCTGGCTCTGCTGAGCGGGCCCTTGTAGTCCCCCAGCTGCTCTGCGGACCC 240

Db 434 ATCTCTGGCTCTGCTGAGCGGGCCCTTGTAGTCCCCCAGCTGCTCTGCGGACCC 493

QY 241 TGGGTGTGGAGTGGTCCGGCTGCTTCTTCTCCG-CCGCTGCCGGATTGCTCCA 299
DB |||||
494 TGGGTGTGGAGTGGTCCGGCTGCTTCTTCCGCGCGTGGCGGATTGCTCCA 553
QY 300 GCGCTGTGGA-GCTGTGTGCGGGATGAGCCCCCTGCTGTCTACTAGGACT-CCACT 357
DB |||||
554 GCGCTGTGAGGCCGTGTGTGCGGGATGAGCCCCCTGCTGTCTACTAGGACTCCCACT 613
QY 358 GAGGGACTGCTGAAGCCAACTGG-GCCAAAGAGCAATGAGTGGCCCCCAGCCCTGA 416
DB |||||
614 GAGGGACTGCTGAAGCCAACTGGTGC AAGAGCAATGAGTGGCCCCCAGCCCTGA 673
QY 417 TCGTGACCCCCCAG-CCGCGGGATGGCCA--GGGGCTCAAGTCAACCATGGGCAGCA 472
DB |||||
674 TGTGACACCCCAAGACCGCGGGATGGCCAGCGGGCTGCAAGTCAACCATGGGCAGCA 733
QY 473 GCTTCAGCTACCCCGATGTTAAGCTCAAAAGGCATCCCTGTGTATCCCTACCCGAG-GGCC 531
DB |||||
734 GCTTCAGCTACCCCGATGTTAAGCTCAAAAGGCATCCCTGTGTATCCCTACCCGAGAGGCC 793
QY 532 ACCTCCCAAGCCCTGATGCGACTCTCTGCTGAAGGAGCCACTGGCCGATCCCCACCC 591
DB |||||
794 ACCTCCCAAGCCCTGATGCGACTCTCTGCTGAAGGAGCCACTGGCCGATCCCCACCC 853
QY 592 ATGGCA-CACAGCTGCCAGCACCTTTGCCAGTAGTCTCGTGGCTCCGAGGAGTACTA 650
DB |||||
854 ATGGAGACAGCTGCCAGCACCTTTGCCAGTAGTCTCGTGGCTCCGAGGAGTACTA 913
QY 651 TTCTTTCCATGATCGGACTCGACCTGGACCTGCCGAGATGGGAGTGGCTCCATGTCCAGCGC 710
DB |||||
914 TTCTTTCCATGATCGGACTCGACCTGGACCTGCCGAGATGGGAGTGGCTCCATGTCCAGCGC 973
QY 711 AGAAATTGATGTCTCATCTTCAAGAGCTGACAGA-GCTGTTTCAGCGTACACAGATCG 769
DB |||||
974 AGAAATTGATGTCTCATCTTCAAGAGCTGACAGAGGCTGTTTCAGCGTACACAGATCG 1033
QY 770 ATGAGCTGCCAAGTGCATCAGACACTGTGTTCTCGAGAGAAGCCAGTAAGATCTCGG 829
DB |||||
1034 ATGAGCTGCCAAGTGCATCAGACACTGTGTTCTCGAGAGAAGCCAGTAAGATCTCGG 1093
QY 830 ACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGGCGCGC 889
DB |||||
1094 ACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGGCGCGC 1153
QY 890 TGGTACCGCGGATCATTCGCAATTAGTACCCGAAAGAGCCGTGCTGCCCAAGACCTCGG 949
DB |||||
1154 TGGTACCGCGGATCATTCGCAATTAGTACCCGAAAGAGCCGTGCTGCCCAAGACCTCGG 1213
QY 950 AGGGTGGTTCAACTCGGGCTGTGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGA 1009
DB |||||
1214 AGGGTGGTTCAACTCGGGCTGTGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGA 1273
QY 1010 CCATGGTGGGCTCAGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCCAAGGAGACGA 1069
DB |||||
1274 CCATGGTGGGCTCAGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCCAAGGAGACGA 1333
QY 1070 CTGCAAGTCCATTCGCCCGGAAGCTGAGCGCTTATGGAAGCTCCAGGGTACCAGCAAGCC 1129
DB |||||
1334 CTGCAAGTCCATTCGCCCGGAAGCTGAGCGCTTATGGAAGCTCCAGGGTACCAGCAAGCC 1393
QY 1130 ATGACTCATCTTCCAGGGCACCGACACAGACTCGTTCGGGGGCACCTGTGCTCCAGGTCT 1189
DB |||||
1394 ATGACTCATCTTCCAGGGCACCGACACAGACTCGTTCGGGGGCACCTGTGCTCCAGGTCT 1453
QY 1190 ACTGTCAACCTTCGCCAGGCCAGCTGCCACACCTTTCTGGGAGAAGCATGCGCTTACAG 1249
DB |||||
1454 ACTGTCAACCTTCGCCAGGCCAGCTGCCACACCTTTCTGGGAGAAGCATGCGCTTACAG 1513
QY 1250 ATGAAGAGGGGACAGAGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGGCCACT 1309
DB |||||
1514 AATGAAGAGGGGACAGAGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGGCCACT 1573

QY 1310 CTGGCTCCTCTGCTGCTGGCTGACTGGGTTCCTGGACCATGTGCATTTTCACTGGGCCATG 1369
DB |||||
1574 CTGGCTCCTCTGCTGCTGGCTGACTGGGTTCCTGGACCATGTGCATTTTCACTGGGCCATG 1633
QY 1370 GGATCTAATCTCTCTTGCATCCCAAGCTGGTCTGATCCCTGCCAGGGCCCCCTTCTCTCT 1429
DB |||||
1634 GGATCTAATCTCTCTTGCATCCCAAGCTGGTCTGATCCCTGCCAGGGCCCCCTTCTCTCT 1693
QY 1430 GCTCATGGTCTTTCAGTGGCCCTGATCATGGAAGTAAAGAGTTAGGCAATTACCTTCTGGG 1489
DB |||||
1694 GCTCATGGTCTTTCAGTGGCCCTGATCATGGAAGTAAAGAGTTAGGCAATTACCTTCTGGG 1753
QY 1490 AGTGAACCCCTGACTCCATCCCTTATTCACACCTTAAACCAATCATGCATACTTCCCTC 1549
DB |||||
1754 AGTGAACCCCTGACTCCATCCCTTATTCACACCTTAAACCAATCATGCATACTTCCCTC 1813
QY 1550 CTGGGGTAAATTCACAGTTAAAGAGCTTATCTTAATGATTTGTTATGGGGGTGGG 1609
DB |||||
1814 CTGGGGTAAATTCACAGTTAAAGAGCTTATCTTAATGATTTGTTATGGGGGTGGG 1873
QY 1610 CAGGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCCTGGCTGATGTTCTGTAT 1669
DB |||||
1874 CAGGGCCCACTCTATGTTATGTTAAGGAGTTGGTTCCTGGCTGATGTTCTGTAT 1933
QY 1670 CTTAAACATGACCACAGTTTGTAAAGTACCTCGGCCCGGACCAAGC 1713
DB |||||
1934 CTTAAACATGACCACAGTTTGTAAAGTACCTCGGCCCGGACCAAGC 1977

RESULT 5
ABX92014

ID ABX92014 standard; cDNA; 1977 BP.

XX AC ABX92014;

XX DT 08-MAY-2003 (first entry)

XX DE Lung specific nucleic acid (LSNA) #56.

XX KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
cancer monitoring; cancer staging; cancer imaging; lung cancer;
non-cancerous diseases of the lung; transgenic animal; gene; ss.

XX OS Homo sapiens.

XX PN WO200268633-A2.

XX PD 06-SEP-2002.

XX PF 21-NOV-2001; 2001WO-US043612.

XX PR 22-NOV-2000; 2000US-0252500P.

XX PA (DIAD-) DIADEXUS INC.

XX PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;

XX DR WPI; 2002-713376/77.

XX PT New isolated human nucleic acid molecule and polypeptide, useful for
identifying, diagnosing, monitoring, staging, imaging and treating lung
cancer and non-cancerous diseases of the lung.

XX PS Claim 1; Page 205-206; 389pp; English.

XX CC The invention describes an isolated human nucleic acid (I) encoding any
of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the

KW cytostatic; neoplasm; gene; ss.
XX Homo sapiens.
XX WO2005049806-A2.
XX 02-JUN-2005.
XX 11-MAR-2004; 2004WO-US007412.
XX 14-MAR-2003; 2003US-00389559.
XX (NUVE-) NUVELO INC.
XX Tang TY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;
XX Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;
XX Wehrman T, Weng G, Boyle B;
XX WPI; 2005-417730/42.
XX P-PSDB; AEA20112.
XX New polynucleotide encoding a polypeptide with biological activity,
XX useful for treating a disease or disorder, e.g. osteoarthritis, burns,
XX CNS and peripheral disease, stroke, autoimmune disorders, viral
XX infection, or cancer.
XX Claim 1; SEQ ID NO 239; 500pp; English.
XX The invention describes a new isolated polynucleotide (I) encoding a
XX polypeptide with biological activity comprising: a nucleotide sequence of
XX SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes
XX to the sequence of (I) under stringent hybridization conditions; or a
XX nucleotide sequence having greater than 99% sequence identity with the
XX sequence of (I). Also described are: a(n) (expression)vector comprising
XX (I); a host cell genetically engineered to comprise (I) operatively,
XX associated with a regulatory sequence that modulates expression of the
XX polynucleotide in the host cell; an isolated polypeptide comprising a
XX sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
XX is a polypeptide encoded by (I); or a polypeptide encoded by a
XX polynucleotide hybridizing under stringent conditions with any one of SEQ
XX ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
XX carrier; an antibody directed against the polypeptide of (3); a method
XX for detecting (I) in a sample; a method for detecting the polypeptide of
XX (3) in a sample; a method for identifying a compound that binds to the
XX polypeptide of (3); a method of producing the polypeptide of (3); and a
XX collection of polynucleotides, where the collection comprising of at
XX least one of SEQ ID NOS: 1-567. (I) is a polynucleotide comprising any of
XX the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
XX activity, which comprises any of the amino acid sequence of SEQ ID NOS:
XX 568-1134. All sequences are fully defined in the specification. The
XX sequences and methods are useful in diagnostics, forensic, and gene
XX mapping, in identifying of mutations responsible for genetic disorders or
XX other traits, in assessing biodiversity, and for producing many other
XX types of data and products dependent on DNA and amino acid sequences. The
XX composition and method are useful for treating a disease or disorder,
XX e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
XX peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
XX autoimmune disorders, viral infection, or cancer. This sequence encodes a
XX novel polypeptide of the invention.
XX Sequence 791 BP; 149 A; 278 C; 222 G; 142 T; 0 U; 0 Other;
Query Match 44.5%; Score 763; DB 14; Length 791;
Best Local Similarity 99.7%; Pred. No. 7.1e-196;
Matches 785; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 ATGCCCGCCCTGGACACCCGCCCGCCGATCTGGGCTCCAGCTTGGGACCGTGGGAG 60
DB 1 ATGCCCGCCCTGGACACCCGCCCGCCGATCTGGGCTCCAGCTTGGGACCGTGGGAG 60
QY 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAAACCACTTCAGCCCCCAACGCGC 120
DB 61 CGG-CAACAGAGCTATGTCTGGAGACATATGATAAAACCACTTCAGCCCCCAACGCGC 119

QY	121	CGCACCCGTAGACACAGACCCCAAGGACCCCTGGCCACCATGGGCCAGAGACATTACCTTC	180
DB	120	CGCACCCGTAGACACAGACCCCAAGGACCCCTGGCCACCATGGGCCAGAGACATTACCTTC	179
QY	181	ATCTCTGGCTGTGCTGAGCCGCCCTTTGAGTCCCCACACCTGTGCTGTCTGGCGACCC	240
DB	180	ATCTCTGGCTGTGCTGAGCCGCCCTTTGAGTCCCCACACCTGTGCTGTCTGGCGACCC	239
QY	241	TGGGTGTGGAGTGTGTCGGGCTGCTTCTGCTTCCGCGCTGCGGGATTCCTCCAG	300
DB	240	TGGGTGTGGAGTGTGTCGGGCTGCTTCTGCTTCCGCGCTGCGGGATTCCTCCAG	299
QY	301	CGCTGTGAGAGCTGTGTGGGATGCGAGCCCTGCTCTCTACTGAGCACTCCACTGAG	360
DB	300	CGCTGTGAGAGCTGTGTGGGATGCGAGCCCTGCTCTCTACTGAGCACTCCACTGAG	359
QY	361	GGGACTGTCTGAAGCAACTGGGCCCAAGGAGCAATGGAGTGTGCCCCCAGCCCTGATCT	420
DB	360	GGGACTGTCTGAAGCAACTGGGCCCAAGGAGCAATGGAGTGTGCCCCCAGCCCTGATCT	419
QY	421	GCACCCCGCAGCCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGCGAGCATTTCAGC	480
DB	420	GCACCCCGCAGCCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGCGAGCATTTCAGC	479
QY	481	TACCCCGATGTTAAGCTCAAGGCAATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA	540
DB	480	TACCCCGATGTTAAGCTCAAGGCAATCCCTGTGTATCCCTACCCGAGGGCCACCTCCCCA	539
QY	541	GCCCTGTATGCGGACTCTCTGTGCAAGGAGCCACTGGCCGATCCCCCAACCCATGCGAC	600
DB	540	GCCCTGTATGCGGACTCTCTGTGCAAGGAGCCACTGGCCGATCCCCCAACCCATGCGAC	599
QY	601	AGCTGCCCAGACACTTTGCCAGTAGTCTCTGTGGTCCGAGGAGTACTATTCTTTCCAT	660
DB	600	AGCTGCCCAGACACTTTGCCAGTAGTCTCTGTGGTCCGAGGAGTACTATTCTTTCCAT	659
QY	661	GAGTGGGACCTGGACCTGCGCGAGATGGGAGTGGCTTCCATGTGAGCCGAGAAAATTGAT	720
DB	660	GAGTGGGACCTGGACCTGCGCGAGATGGGAGTGGCTTCCATGTGAGCCGAGAAAATTGAT	719
QY	721	GTGCTCATCTTCAAGAAGCTGACAGA-GCTTTACGCGTACACCATCGATGAGTGGC	779
DB	720	GTGCTCATCTTCAAGAAGCTGACAGAAGGCTGTTACAGCGTACACCATCGATGAGTGGC	779
QY	780	CAAGTGC 786	
DB	780	CAAGTGC 786	
RESULT 7			
ABT07645			
ID	ABT07645	standard; cDNA; 654 BP.	
XX	ABT07645;		
XX	ABT07645;		
DT	14-NOV-2002	(first entry)	
XX	Human breast cancer associated coding sequence SEQ ID NO: 124.		
XX	Human; breast specific gene; breast specific protein; breast cancer;		
KW	Human; breast specific gene; breast specific protein; breast cancer;		
KW	gene therapy; cytostatic; gene; ss.		
OS	Homo sapiens.		
XX	WO200264611-A1.		
PD	22-AUG-2002.		
XX	12-FEB-2002; 2002WO-US004197.		
XX	13-FEB-2001; 2001US-0268292P.		
XX			

QY 61 CGGCAACAGAGCTATCTGGAGACATATGATAAACCACCTCAGCCGCCACACGAGCGC 120
DB 140 CGGCCAACAGAGCTATCTGGAGACATATGATAAACCACCTCAGCCGCCACACGAGCGC 199
QY 121 CGCAACCCGTAGACAGACACCCCAAGGACCCTGGCCACCATGGCCAGAGAGCATTTACCTTC 180
DB 200 CGCACCCGTAGACAGACACCCCAAGGACCCTGGCCACCATGGCCAGAGAGCATTTACCTTC 259
QY 181 ATCTCTGGCTCTGCTAGAGCGGCGCCCTTGAAGTCCCCACCTGCTGCTCTGCGGACCC 240
DB 260 ATCTCTGGCTCTGCTAGAGCGGCGCCCTTGAAGTCCCCACCTGCTGCTCTGCGGACCC 319
QY 241 TGGGTGTGGAGAGTGGTCCGGGCTGCTCTGCTTCCGCGCTGCTCCGGGATTCCTTCAG 300
DB 320 TGGGTGTGGAGAGTGGTCCGGGCTGCTCTGCTTCCGCGCTGCTCCGGGATTCCTTCAG 379
QY 301 CGCTGTGGAGCTGTGTGGGAGATGAGCGCCCTGCGCTGCTACTGAG 348
DB 380 CGCTGTGGAGCTGTGTGGGAGATGAGCGCCCTGCGCTGCTACTGAG 427

RESULT 14

AAZ13392
ID AAZ13392 standard; cDNA; 300 BP.

XX AAZ13392;

AC
XX
DT 12-OCT-1999 (first entry)

XX Human gene expression product cDNA sequence SEQ ID NO:861.

XX Human; gene; gene expression product; diagnosis; therapy; probe;
KW detection; mapping; tissue typing; profiling; forensic; cancer;
KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
XX Homo sapiens.

XX WO9938972-A2.

XX 05-AUG-1999.

XX 28-JAN-1999; 99WO-US001619.

XX 28-JAN-1998; 98US-0072910P.

PR 24-FEB-1998; 98US-0075954P.

PR 31-MAR-1998; 98US-0080114P.

PR 03-APR-1998; 98US-0080515P.

PR 03-APR-1998; 98US-0080666P.

PR 21-OCT-1998; 98US-0105234P.

PR 28-OCT-1998; 98US-0105877P.

XX (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.

XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX
XX WPI; 1999-494092/41.

XX Novel human genes and their expression products which are differentially
PT expressed in different cell types.
PT
XX
XX Claim 1; Page 860; 2479pp; English.

PS
XX The present invention describes a library of human polynucleotides

CC comprising the sequences given in AAZ12532 to AAZ17779. Also described is
CC a method of detecting differentially expressed genes correlated with the
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample from a cell
CC suspected of being cancerous, where the gene product is encoded by one of
CC the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The

CC polynucleotides can be used as a source of primers and probes, which can
CC be used for a variety of purpose, e.g. detection of expression levels,
CC mapping, tissue typing or profiling, forensics, genetic analysis and
CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC can be used for raising antibodies for experimental, diagnostic and
CC therapeutic purposes. The polynucleotides may also be used to construct
CC arrays for diagnostics (which may be used to determine function of an
CC encoded protein); and to detect differences in expression levels between
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC identify a genetic predisposition or susceptibility to a disease such as
CC cancer). The polynucleotides of the invention are especially used in the
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC and lung cancer. The polynucleotides can also be used to screen for
CC peptide analogues and antagonists

XX
SQ Sequence 300 BP; 63 A; 96 C; 90 G; 51 T; 0 U; 0 Other;

Query Match 17.5%; Score 300; DB 2; Length 300;

Best Local Similarity 100.0%; Pred. No. 1.1e-70;

Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 825 CTCGACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGG 884

DB 1 CTCGACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGG 60

QY 885 CGCCTGTGTACGGCGCATCTTCGATTTAGTACCCGAAAGAGCGGTCTGCCCCACAGAC 944

DB 61 CGCCTGTGTACGGCGCATCTTCGATTTAGTACCCGAAAGAGCGGTCTGCCCCACAGAC 120

QY 945 CTCGGAGGCTGCTCACTCGGGCTGCTGCCCAACCGCTGCTGCCCTGACAGTGCCCA 1004

DB 121 CTCGGAGGCTGCTCACTCGGGCTGCTGCCCAACCGCTGCTGCCCTGACAGTGCCCA 180

QY 1005 TGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGTGCACAGTGAGATCTCCACAGGA 1064

DB 181 TGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATGAGTGCACAGTGAGATCTCCACAGGA 240

QY 1065 GACGACTGCAGATGCCATGCCCGGAGCTTGAGGCTTTATGGAGCTCCAGGGTACCAGC 1124

DB 241 GACGACTGCAGATGCCATGCCCGGAGCTTGAGGCTTTATGGAGCTCCAGGGTACCAGC 300

RESULT 15

AAZ98308

ID AAZ98308 standard; cDNA; 300 BP.

XX AAZ98308;

XX 24-SEP-1999 (first entry)

XX Human cancer cell derived cDNA #34.

XX Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
KW integral membrane protein; aspartyl protease; GATA family; wnt family;
KW transcription factor; G-protein alpha subunit; protein phosphatase;
KW phospholipase binding protein; diacylglycerol binding protein; trypsin;
KW protein kinase; tyrosine phosphatase; developmental signalling protein;
KW WWP domain; therapy; forensic; genetic mapping; diagnostic;
KW detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
KW Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
KW leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
KW prostate; ss.

XX Homo sapiens.

XX WO9933982-A2.

XX 08-JUL-1999.

XX 22-DEC-1998; 98WO-US027610.

XX 23-DEC-1997; 97US-0068755P.

PR 03-APR-1998; 98US-0080664P.

Db 241 CCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATG 300
Search completed: March 12, 2006, 04:23:06
Job time : 1066 secs

PR 21-OCT-1998; 98US-0105234P.
PR 27-OCT-1998; 98US-0105877P.
PR 21-DEC-1998; 98US-00217471.
XX
XX (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
PA
XX
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamon G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
XX
XX WPI; 1999-430243/36.
DR
XX
XX New isolated human polynucleotides.
PT
XX
XX Claim 1; Page 326; 591pp; English.
XX
XX This invention describes novel isolated human polynucleotides obtained by
CC screening for differential expression in colon cancer, breast cancer and
CC lung cancer cell lines. The polynucleotides of the invention are
CC represented in AA98275-X99118 and encode polypeptides of protein
CC families selected from 4 transmembrane segments integrated with various
CC proteins, 7 transmembrane receptors, ATPases associated with various
CC cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC transcription factors, G-protein alpha subunit, phospholipase C,
CC diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
CC protein tyrosine phosphatase, trypsin, wnt family of developmental
CC signalling proteins and WW/zsp5/WWP domain containing proteins. The
CC encoded polypeptides also have a functional domain selected from Ank
CC repeat, basic region plus leucine zipper transcription factors,
CC bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger
CC (C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease
CC domain. The polynucleotides encode polypeptides with similarity to known
CC protein families and are predicted to have similar properties. The novel
CC polynucleotides can be used to develop products for use as therapeutic
CC agents and in forensics, genetic analysis, mapping and diagnostic
CC applications. In particular, the product can be used for the detection
CC and management of cancers. They can be used for treating e.g. cervical
CC cancers, melanomas, colorectal adenocarcinomas, Wilms tumor, sarcomas,
CC retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
CC myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
CC myeloid leukemia, and lymphomas such as histiocytic lymphoma, anhydric
CC hereditary ectodermal dysplasia, congenital alveolar dysplasia, and
CC epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
CC mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
CC prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC the skin
XX
XX Sequence 300 BP; 68 A; 90 C; 86 G; 56 T; 0 U; 0 Other;
Query Match 17.4%; Score 298.4; DB 2; Length 300;
Best Local Similarity 99.7%; Pred. No. 3e-70;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 740 TCACAGAGCTGTCACGCTACACAGATCGATGAGTGGCCAGTGCACATCAGACACTG 799
DB 1 TCACAGAGCTGTCACGCTACACAGATCGATGAGTGGCCAGTGCACATCAGACACTG 60
QY 800 TGTTCCTGGAGAGACAGTACAGATCTCGGACCTTATCAGCAGCATCAGCAGGACTACC 859
DB 61 TGTTCCTGGAGAGACAGTACAGATCTCGGACCTTATCAGCAGCATCAGCAGGACTACC 120
QY 860 ACTGATGAGCAGGATGCTGAGGGCGCGCTGTGTAGCGGGCATTCATTCGATGATACCC 919
DB 121 ACTGATGAGCAGGATGCTGAGGGCGCGCTGTGTAGCGGGCATTCATTCGATGATACCC 180
QY 920 GAAAGAGCGTGTCTCGCCACACAGCTCGAGGGTGTCTCACTCGGGGTGTCGCCCAA 979
DB 181 GAAAGAGCGTGTCTCGCCACACAGCTCGAGGGTGTCTCACTCGGGGTGTCGCCCAA 240
QY 980 CCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTGGGCTCAGGTCTCAGCCAGGATG 1039

GenCore version 5.1.7
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Run on: March 11, 2006, 19:52:41 ; Search time 6305 Seconds
(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8:	gb_est7:*
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11:	gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1451.2	84.7	1671	4	CR749558	CR749558 Homo sapi
2	1197	69.9	1197	11	DQ045548	DQ045548 Homo sapi
3	1145	66.8	1181	11	DQ045549	DQ045549 Pan trogl
4	951.8	55.6	1657	4	AK007551	AK007551 Mus muscu
5	803.6	46.9	975	3	BM460277	BM460277 AGENCOURT
6	791	46.2	1596	4	AK051860	AK051860 Mus muscu
7	731.4	42.7	753	7	CN289134	CN289134 170005999
8	687	40.1	917	5	BQ691555	BQ691555 AGENCOURT
9	679.6	39.7	1009	5	BY07606	BY07606 BX707606
10	669.4	39.1	1015	2	BE741035	BE741035 601594018
11	647	37.8	966	2	BE901537	BE901537 601677420
12	622	36.3	622	3	BM823479	BM823479 K-EST0094
13	577.8	33.7	582	3	BP315176	BP315176 BP315176
14	576.2	33.6	826	3	BI694617	BI694617 603347838
15	540.2	31.5	583	3	BP331524	BP331524 BP331524
16	526.6	30.7	556	1	AA573775	AA573775 NK07610.8
17	510	29.8	510	1	AA316608	AA316608 EST188290
18	496.4	29.0	783	7	CK478920	CK478920 AGENCOURT
19	489.2	28.6	984	2	BF135747	BF135747 601781110
20	480.2	28.0	489	1	AI925416	AI925416 wc30802.x
21	476	27.5	1040	3	BI411303	BI411303 602964692
22	470.6	27.8	680	3	BI653517	BI653517 603300520

23	469.2	27.4	677	10	AG071555	AG071555 Pan trogl
24	459.2	26.8	537	2	BF191474	BF191474 239074 MA
25	455.8	26.6	513	6	CD702656	CD702656 EST19181
26	450.2	26.3	470	5	BX110746	BX110746 BX110746
27	441.8	25.8	825	8	DN936585	DN936585 AGENCOURT
28	441.6	25.8	944	3	BI905189	BI905189 603167516
29	410.6	24.0	746	3	BI905713	BI905713 603166180
30	410	23.9	535	5	BQ566109	BQ566109 g152a07.y
31	406	23.7	930	3	BI413848	BI413848 602991514
32	402	23.5	423	1	AW008047	AW008047 wv48h06.x
33	395.6	23.1	623	2	BE741110	BE741110 601593919
34	394	23.0	586	2	BG082830	BG082830 H3081C02-
35	394	23.0	756	2	BG871324	BG871324 602792482
36	389.2	22.7	763	10	AG603040	AG603040 Mus muscu
37	384.2	22.4	609	2	BE533148	BE533148 601235445
38	381.8	22.3	918	2	BF144315	BF144315 601787134
39	375	21.9	412	1	AI216202	AI216202 qm37e07.x
40	370	21.6	370	1	AW589267	AW589267 xg27g07.x
41	363.2	21.2	769	7	CK473171	CK473171 AGENCOURT
42	355	20.7	722	3	BI409054	BI409054 602961119
43	345.6	20.2	488	1	AI669760	AI669760 tui2h08.x
44	345.2	20.2	738	2	BI078885	BI078885 602873115
45	341.2	19.9	491	1	AA856355	AA856355 vw99g12.x

ALIGNMENTS

RESULT 1	CR749558	1671 bp	mRNA	linear	HTC 19-AUG-2004
LOCUS	CR749558	Homo sapiens mRNA; cDNA DKFZp686B17277 (from clone DKFZp686B17277).			
DEFINITION	CR749558	HTC			
ACCESSION	CR749558	GI:51476784			
VERSION	CR749558.1				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1671)				
AUTHORS	Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.				
CONSRMT	The German CDNA Consortium				
TITLE	Direct Submission				
JOURNAL	Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY				
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing Consortium of the German Genome Project. This clone (DKFZp686B17277) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/ci.cgi?CloneID=DKFZp686B17277 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.				
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		PDPKDPHGHGPESTIFISGSABPALESPTCLRLTPLRGLKPTGRSTMECPALIVH			
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		TACPAPLPVVLVAPRSTILMSRSTWTCRRWAVAPCRABKLMCSSRS"			
ORIGIN					
Query Match		84.7%; Score 1451.2; DB 4; Length 1671;			
Best Local Similarity		92.9%; Pred. No. 0;			
Matches 1581; Conservative		0; Mismatches 3; Indels 118; Gaps 1;			
QY	1	ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG	60		
DB	69	ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG	128		
QY	61	CGGCCAAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCAACCAAGCGCG	120		
DB	129	CGGCCAAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCAACCAAGCGCG	188		
QY	121	CGCACCCGTAGACAGACACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCAATTACCTTC	180		
DB	189	CGCACCCGTAGACAGACACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCAATTACCTTC	248		
QY	181	ATCTCTGGCTCTGCTGAGCGCGGCCCTTGTAGTCCCCACCTGTGCTCTTGGCGGACCC	240		
DB	249	ATCTCTGGCTCTGCTGAGCGCGGCCCTTGTAGTCCCCCA	285		
QY	241	TGGGTGTGGAGTGTGTGCGGGCTGCCCTTGTCTTCCGCGCTGCGGGATGTGCTCCAG	300		
DB	286	-----	285		
QY	301	CGTGTGGAGCCTGTGTGCGGGATGCGACCCCTGCTCTACTGAGGACTCCACTGAG	360		
DB	286	-----CCTGTCTACTGAGGACTCCACTGAG	310		
QY	361	GGGACTGTGAAGCCAACTGGGCCAAGGAGCACAAATGGAGTGGCCCCCAGCCCTGATCGT	420		
DB	311	GGGACTGTGAAGCCAACTGGGCCAAGGAGCACAAATGGAGTGGCCCCCAGCCCTGATCGT	370		
QY	421	GCACCCCCAGCGCGGGGATGGCCAGCGGCTCAAGTCAACCATGGCGAGCAGCTTCAGC	480		
DB	371	GCACCCCCAGCGCGGGGATGGCCAGCGGCTCAAGTCAACCATGGCGAGCAGCTTCAGC	430		
QY	481	TACCCCGATGTTAAGCTCAAAAGGCATCCTGTGTATCCCTTACCCGAGGGCCACCTCCCA	540		
DB	431	TACCCCGATGTTAAGCTCAAAAGGCATCCTGTGTATCCCTTACCCGAGGGCCACCTCCCA	490		
QY	541	GCCCTCATCGGACTCTCTGCAAGGAGGCACATGGCCGATCCCCACCCATCGGACAC	600		
DB	491	GCCCTCATCGGACTCTCTGCAAGGAGGCACATGGCCGATCCCCACCCATCGGACAC	550		
QY	601	AGCCTGCCAGCACCTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTCCAT	660		
DB	551	AGCCTGCCAGCACCTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTCCAT	610		
QY	661	GAGTCGGAACCTGGACCTGCGGAGATGGGCAGTGGCTCCATGTGCGAGCCGAGAAATTGAT	720		
DB	611	GAGTCGGAACCTGGACCTGCGGAGATGGGCAGTGGCTCCATGTGCGAGCCGAGAAATTGAT	670		
QY	721	GTGCTCATCTTCAGAGACTGACAGAGCTGTTTCAAGCGTACACAGATCGATGAGCTGGCC	780		
DB	671	GTGCTCATCTTCAGAGAGCTGACAGAGCTGTTTCAAGCGTACACAGATCGATGAGCTGGCC	730		
QY	781	AAGTGACATCAGACACTGTGTTCTCTGGAGAAGACCAAGTAGATCTCGGACCTTATCAGC	840		
DB	731	AAGTGACATCAGACACTGTGTTCTCTGGAGAAGACCAAGTAGATCTCGGACCTTATCAGC	790		
QY	841	AGCATCAGCAGGACTACCACTCTGGATGACAGGATGCTGAGGGCCGCTGGTACGCGGC	900		
DB	791	AGCATCAGCAGGACTACCACTCTGGATGACAGGATGCTGAGGGCCGCTGGTACGCGGC	850		

QY	901	ATCATTTCGATTAGTACCCGAAAGAGCGGTGCTCGCCACAGACCTCGGAGGGTCGTTCA	960		
DB	851	ATCATTTCGATTAGTACCCGAAAGAGCGGTGCTCGCCACAGACCTCGGAGGGTCGTTCA	910		
QY	961	ACTCGGGCTGTGCCCCCAACCGCTGTCGCCCTGACAGTGGCCATGAGACCATGTGGGC	1020		
DB	911	ACTCGGGCTGTGCCCCCAACCGCTGTCGCCCTGACAGTGGCCATGAGACCATGTGGGC	970		
QY	1021	TCAGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC	1080		
DB	971	TCAGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC	1030		
QY	1081	ATCGCCCGGAAGCTCAGGCGCTTATGAGCTCCAGGCTACCCAGCAAGCCATGACTCATCC	1140		
DB	1031	ATCGCCCGGAAGCTCAGGCGCTTATGAGCTCCAGGCTACCCAGCAAGCCATGACTCATCC	1090		
QY	1141	TTCCAGGGCACCGACACAGACTCGTGGGGGACCCCTTGTCTCCAGGTGTACTGCTAAACC	1200		
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QY	1201	CTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGCGCTACAGAAAGAGGG	1260		
DB	1151	CTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGCGCTACAGAAAGAGGG	1210		
QY	1261	GGACCAAGGAAACCCCTGTGGGAGAGCTTAGACTGAAAGCAGTCCCACTCTGGCTCTCC	1320		
DB	1211	GGACCAAGGAAACCCCTGTGGGAGAGCTTAGACTGAAAGCAGTCCCACTCTGGCTCTCC	1270		
QY	1321	TGCTTGGCTGACTGGGTTCTGGACCATGTGCAATTTCACTGGCCATGGGATCTACATC	1380		
DB	1271	TGCTTGGCTGACTGGGTTCTGGACCATGTGCAATTTCACTGGCCATGGGATCTACATC	1330		
QY	1381	TCCTTGCATCCCGAGTGTGTGATCCCTGCCAGGGCCCTTCTCTCTGCTCATGGTCT	1440		
DB	1331	TCCTTGCATCCCGAGTGTGTGATCCCTGCCAGGGCCCTTCTCTCTGCTCATGGTCT	1390		
QY	1441	TCAGTGGCTCATCATGGAAGTAAAGGATTTAGCATTTACCTTCTGGAGTGAACCCCTG	1500		
DB	1391	TCAGTGGCTCATCATGGAAGTAAAGGATTTAGCATTTACCTTCTGGAGTGAACCCCTG	1450		
QY	1501	ACTCCATCCCCCTATTGGCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAT	1560		
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LOCUS					
DEFINITION	Homo sapiens FLJ34633 gene, VIRTUAL TRANSCRIPT, partial sequence,	1197 bp	DNA	linear	GSS 02-JUN-2005
ACCESSION	DQ045548				
VERSION	DQ045548.1				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1197)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,				

```
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(her) PLoS Biol. 3 (6), E170 (2005)
15869325
2 (bases 1 to 1197)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
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Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGCCCGCCCTGGACACCCCGCCGAGCATCTGGGCTCCACGCTTGGAGACGTTGGAG 60
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DB 61 CGGCCAACAGAGCTATGCTGGAGACATATGATAAACCACTCAGCCCCCACCACGCGC 120
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QY 301 CGCTGTGGAGCTGTGTGGGGATGCGACCCCTGCTGCTACTGAGGACTCCACTGAG 360
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DB 421 GCACCCCGAGCGCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCGACGCTTCAGC 480
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DB 721 GTGCTCATCTTCAAGAGCTGACAGAGCTGTTTCAAGGTACACAGATCGATGAGCTGCC 780
QY 781 AAGTCGACATCAGACACTGTGTTCTTGGAGAAGACCAAGATCTCGGACCTTATCAGC 840
DB 781 AAGTCGACATCAGACACTGTGTTCTTGGAGAAGACCAAGATCTCGGACCTTATCAGC 840
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QY 1141 TTCAGGGGACCGACACAGACTGTCGGGGGACCCCTTGTCCAGGTTGACTGCTAA 1197
DB 1141 TTCAGGGGACCGACACAGACTGTCGGGGGACCCCTTGTCCAGGTTGACTGCTAA 1197
RESULT 3
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LOCUS 1181 bp DNA linear GSS 02-JUN-2005
DEFINITION Pan troglodytes FLJ34633 gene, VIRUAL TRANSCRIPT, partial
sequence, genomic survey sequence.
DQ045549
VERSION DQ045549.1 GI:66896764
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE 1 (bases 1 to 1181)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (her) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1181)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source
Location/Qualifiers
1..1181
/organism="Pan troglodytes"
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QY	1	ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCAGCTTGGAGCCGTGGGAG	60		
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QY	61	CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACAACCTCAGCCCCCAACAGCCGC	120		
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QY	181	ATCTCTGGCTCTGCTGAGCGGGCCCTTGAGTCTCCCACTGCTGCTCTGGCGACCC	240		
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Db	601	AGCTGCCAGACACCTTGCAGTAGTCTCTGTTGCTCCTGTTGCTGAGGAGTACTATTCTTCCAT	660		
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LOCUS					
DEFINITION		AK007551 1657 bp mRNA linear HTC 03-APR-2004			
ACCESSION		Mus musculus 10 day old male pancreas cDNA, RIKEN full-length			
VERSION		enriched library, clone:1810019J16 product:SIMILAR TO TATA BOX			
KEYWORDS		BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE II, CI,			
SOURCE		130KD homolog [Mus musculus], full insert sequence.			
ORGANISM		AK007551			
REFERENCE		AK007551.1 GI:12841167			
AUTHORS		HTC; CAP trapper.			
TITLE		Mus musculus (house mouse)			
JOURNAL		Mus musculus			
PUBMED		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE		Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;			
AUTHORS		Sciurognathi; Muridae; Murinae; Mus.			
TITLE		1 Carninci, P. and Hayashizaki, Y.			
JOURNAL		High-efficiency full-length cDNA cloning			
PUBMED		Meth. Enzymol. 303, 19-44 (1999)			
REFERENCE		2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,			
AUTHORS		Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE		Normalization and subtraction of cap-trapper-selected cDNAs to			
JOURNAL		prepare full-length cDNA libraries for rapid discovery of new genes			
PUBMED		Genome Res. 10 (10), 1617-1630 (2000)			
REFERENCE		3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,			
AUTHORS		Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,			
TITLE		Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A.,			
JOURNAL		Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,			
PUBMED		Fujiwaka, S., Inoue, K., Togawa, X., Izawa, M., Ohara, E., Watahiki, M.,			
REFERENCE		Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, G.,			
AUTHORS		Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE		RIKEN integrated sequence analysis (RISA) system--384-format			
JOURNAL		sequencing pipeline with 384 multipicapillary sequencer			
PUBMED		Genome Res. 10 (11), 1757-1771 (2000)			
REFERENCE		4 The RIKEN Genome Exploration Research Group Phase II Team and the			
AUTHORS		PANTOM Consortium.			
TITLE		Functional annotation of a full-length mouse cDNA collection			
JOURNAL		Nature 409, 685-690 (2001)			
PUBMED		5 The FANTOM Consortium and the RIKEN Genome Exploration Research			
REFERENCE		Group Phase I & II Team.			
AUTHORS		Analysis of the mouse transcriptome based on functional annotation			
TITLE		of 60,770 full-length cDNAs			
JOURNAL		Nature 420, 563-573 (2002)			
PUBMED		6 (bases 1 to 1657)			
REFERENCE		Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,			
AUTHORS		Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,			
TITLE		Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,			

Hiraka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kaesawa, T., Kato, H., Kawaji, J., Kojima, Y., Konno, H., Kouda, M., Koyasu, T., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saïto, H., Saïto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGGAGGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trnaase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter of sequence[5', GAGAGAGAGCGCGCAATTAATTCGATTAATTAATTAATCCGCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLA.

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mutative"

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CDs

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ORIGIN

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QY	61	CGGCCAACAGAGCTATGCTCTGGAGACATATGATAAACACGCTCAGCGCCCCACCAAGCCGC	120		
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[illegible]


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BM460277.1 GI:18509317
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Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 975)
NIH-MGC http://mgi.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 659.
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/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

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Best Local Similarity 98.5%; Pred. No. 2e-195;
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QY 667 GACCTGGACCTGCCGAGATGGGCAGTGGCTCATGTGAGCGCGAATAATGATGTGCTC 726
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DEFINITION enriched library, Clone:D23001M17 product:hypothetical protein,
full insert sequence.
AK051860
AK051860.1 GI:26342255
VERSION HTC; CAP trapper.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE Carninci, P. and Hayashizaki, Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 10349636
PUBMED
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
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Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
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11042159

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Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

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The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

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Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

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AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

REFERENCE
AUTHORS

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

FEATURES
source

Location/Qualifiers
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CDS

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Best Local Similarity 85.8%; Pred. No. 3.8e-192;
Matches 891; Conservative 0; Mismatches 145; Indels 3; Gaps 1;
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Directionally cloned into EcoRI/XhoI sites using the
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Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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RESULT 9
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DEFINITION
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EST 16-DEC-2002
EST 10 day old male pancreas Mus
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
PUBMED
COMMENT

BY707606 GI:27118783
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Mus musculus (house mouse)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dregani, T.A.,
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Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
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Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
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Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
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Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kitahara, T., Konno, H., Nakamura, M.,
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Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12456851
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for

FEATURES		Location/Qualifiers	source
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DB	344	CGCTGTGGGGCTTGTGTGGGGGCTGCAGCCCTGCAATTGTCTGCGGAGACCCCATTTGA	403
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QY	780	CAAGTGACATCAGACACTGTGTCTCTGGAGAGACCAAGTAAAGATCTCGGACCTTATCAG	839

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QY	840	CAGCATCAGCAGGACTACCACTCGATCAGCAGATGCTGAGGGCCGCTGTGTACGCG	899
Db	884	CAGCATCAGCAGGACTACCACTCGATGATGAGCA-GACGCCGAGGGCCGCTG--TCGGG	940
QY	900	CATCATTCGCATTAGTACCCGAAAGAGCGTCTCGCCCCACAGACCTCCGAGGGGTC	955
Db	941	GATCATCCGTATTAGTATGCAAAAGCTGCTCGGCCACAGACTCCGAGGGGGTC	996

RESULT 10

BE741035

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BE741035

601594018F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947861 5',

1015 bp mRNA linear EST 15-SEP-2000

mrna sequence.

BE741035

BE741035.1 GI:10155027

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1015)

NIH-MGC <http://mgi.nhl.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM810 row: d column: 06

High quality sequence stop: 752.

Location/Qualifiers

1..1015

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3947861"

/tissue_type="adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_9"

/note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match

Best Local Similarity

Matches 837; Conservative 0; Mismatches 66; Indels 18; Gaps 11;

QY	63	GCACAAGAGCTATGTCTGGAGACATATGATAAACCACTCTAGCCGCCACCAAGCGCG	122
DB	9	GCACAAGAGCTATGTCTGGAGACATATGATAAACCACTCTAGCCGCCACCAAGCG-CG	67
QY	123	CACCCGTAGACAGACCCCAAGGACCTGGCCACCATGGCCAGAGAGCATTTACCTTCAT	182
DB	68	CAACCGTAGACAGACCCCAAGGACCTGG-CACCATGGGCCAGAGAGCATTTACCTTCAT	126
QY	183	CTCTGGCTGTGTAGCCGCGCTTGTAGTCCCGCCACCTGCTGCCTGCTGGGACCTCG	242
DB	127	CTCTGGCTGTGTAGCCGCG-CCTTGTAGTCCCGCCACCTGCTGCCTGCTGGGACCTCG	185

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QY 243 GGTGTGGAGTGGTGGCGGGTGGCTTCTGCTTCCGCGCTGCGGGATTGCCCTCCAGCG 302
Db 186 GGTGTGGAGTGGTGGCGGGTGGCTTCTGCTTCCGCGCTGCGGGATTGCCCTCCAGCG 245
QY 303 CTGTGGAGCCTGTGTGGGGATGACAGCCCTGCTGCTACTAGGACTCCACTGAGGG 362
Db 246 CTGTGGAGCCTGTGTGTGGGGATGACAGCCCTGCTGCTACTAGGATTCCACTGAGGG 305
QY 363 GACTGTGAAGCCAACTGGGGCAAGAGGACAAATGGAGTGGCCCCCGCCCTGATCGTC 422
Db 306 GACTGTGAAGCCAACTGGGGCAAGAGGACAAATGGAGTGGCCCCCGCCCTGATCGTC 365
QY 423 ACCCCGAGCGGGGATGGCCAGCGCTCAAGTCAACATGGGAGGAGCTTCAGCTA 482
Db 366 ACCCCGAGCGGGGATGGCCAGCGCTCAAGTCAACATGGGAGGAGCTTCAGCTA 425
QY 483 CCCCAGATTTAAGCTCAAAAGCATCCCTGTGTATCCCTACCCGAGGCGCACTCCCGAGC 542
Db 426 CCCCAGATTTAAGCTCAAAAGCATCCCTGTGTATCCCTACCCGAGGCGCACTCCCGAGC 485
QY 543 CCTGTATGCGGACTCTGTGCTGAAGAGGACCACTGGCCGATCCCGCCACCCATGGGACACAG 602
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QY 663 GTCCGAGCTGGACTGCGGAGATGGGAGTGGCTCCATGTCCAGCGCGAGAAATTGATGT 722
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QY 723 GCTCATCTTCAAGAAGCTGACAG- AGCTGTTCAGCGTACACAGAT- -CGATGAGCTGG 778
Db 664 GCTCATCTTCAAGAAGCTGACAGAAAGCTGTTCAGGTTACACAGATTTCGATTTGAGCTGG 723
QY 779 CCAAGTGACA-TCAGACACTGTGTTCTG- -GAGAAGACCAAGTAAAGTCTGGACCTT 834
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QY 835 ATCAGCAGCATCAGCAGGACT- -ACCACCTGGATGAGCAGGATGCTGAGGCGCGCTGG 892
Db 784 TATCAGCGATCAGCGCGGATTTACCCCTGGATAGCGAGGTTGAG- -GCCCTG 840
QY 893 TAGCGGCGCATATTGCGATTAGTACCGGAAAGAGCCGTGCTCGGCCACAGACCTCGGAGG 952
Db 841 GTAGCGGCGCATATTGCGATTAGTAAACGACATAGCGGTCCCCCACCAGACCTGAGGGGC 900
QY 953 GTGTTTCAACTCGGGTGTCTG 973
Db 901 GTCAATCGGCTGGCGCCACGG 921

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LOCUS 601677420F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960220 5',
DEFINITION mRNA sequence.
ACCESSION BE901537
VERSION BE901537.1 GI:10390818
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 966)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLC842 row: g column: 05
High quality sequence stop: 668.
Location/Qualifiers
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/clone="IMAGE:3960220"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/notes="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Query Match	Best Local Similarity	Score	647;	DB 2;	Length	966;			
Matches	750;	Conservative	0;	Mismatches	40;	Indels	9;	Gaps	7;
QY 95	AACCACTCAGCCCCCAACCAAGCGCGGCGGACCCGCTAGACACCAACCCCAAGGACCCCTGGCC	154							
Db 1	AACCACTCAGCCCCCAACCAAGCGCGGCGGACCCGCTAGACACCAACCCCAAGGACCCCTGG-C	59							
QY 155	ACCATGGCGCAGAGAGCATTTACCTTCATCTCGCTCTGCTGAGCGCGCCCTTCAGTCCC	214							
Db 60	ACCATGGCGCAGAGAGCATTTACCTTCATCTCGCTCTGCTGAGCGCGCCCTTCAGTCCC	119							
QY 215	CAACCTGCTGCTGCTCTGCGCACCCCTGGGTGTGGGAGTGGTGC CGGGTGCCTTCCTGCT	274							
Db 120	CAACCTGCTGCTGCTCTGCGCACCCCTGGGTGTGGGAGTGGTGC CGGGTGCCTTCCTGCT	179							
QY 275	TCGCGCGCTGCGGGATTGCTTCAGGGCTGTGGAGCCTGTGTGCGGGGATGACGCCCT	334							
Db 180	TCGCGCGCTGCGGGATTGCTTCAGGGCTGTGGAGCCTGTGTGCGGGGATGACGCCCT	239							
QY 335	GCCTGTCTACTGAGGACTCCACTGAGGGGAGTCTGAAGCCAACTGGGCCCAAGAGACACA	394							
Db 240	GCCTGTCTACTGAGGACTCCACTGAGGGGAGTCTGAAGCCAACTGGGCCCAAGAGACACA	299							
QY 395	ATGGAGTGGCCCCCAGCCCTGATCGTGACACCCCGCGCGGGATGGCCAGCGGCTCA	454							
Db 300	ATGGAGTGGCCCCCAGCCCTGATCGTGACACCCCGCGCGGGATGGCCAGCGGCTCA	359							
QY 455	AGTCAACCATGGGAGGAGCTTCAGCTACCCCGATGTTAAGCTCAAGGATCCCTGTGT	514							
Db 360	AGTCAACCATGGGAGGAGCTTCAGCTACCCCGATGTTAAGCTCAAGGATCCCTGTGT	419							
QY 515	ATCCCTACCGGAGGGCCACCTCCCGAGCCCTGATGCGGACTCTCTGCTGCAAGAGGCAC	574							
Db 420	ATCCCTACCGGAGGGCCACCTCCCGAGCCCTGATGCGGACTCTCTGCTGCAAGAGGCAC	479							
QY 575	TGGCCGATCCCGCCACCATGCGACACAGCCTGCGCCAGACCTTTTGCAGTAGTCTCGTG	634							
Db 480	TGGCCGATCCCGCCACCATGCGACACAG- CTGCCCAGACCTTTTGCAGTAGTCTCGTG	538							
QY 635	GCTCCGAGGAGTACTATTCTTTCCATGAGTGGAGCTGGAACCTGCGGAGATGGGAGTG	694							
Db 539	GCTCCGAGGAGTACTATTCTTTCCATGAGTGGAGCTGGA- CTGCGGAGATGGGAGTG	597							
QY 695	GCTCCATGTGAGCGCGGAGAAATTGATGTGCTCATCTTCAGAGAGCTGACACA- GCTGCTC	753							
Db 598	G-TCCATGTGAGCGCGGAGAAATTGATGTGCTCATCTTCAGAGAGCTGACACGAGCTGCTTC	656							

QY	754	AGGTTACACCAGA---TCGATGAGCTGGCCAAAGTGCACATTCAGACACTGTGTTCTCTGGAG	810
Db	657	AGGTTACACCAGATCGAATGAAGCTGGCCAGTGCACATTCAGACACTGGTTCCGGAGC	716
QY	811	AAGACAGTAAGATCTTCGGACCTTATCAGCAGCATCACGAGGACTTACCACCTGGATGAG	870
Db	717	AAGACAGTAAGAACTCGGACCTTATTCAGCAGGATACGCAAGAATACCACCGGATGAG	776
QY	871	CAGG-ATGCTGAGGGCCGC	888
Db	777	CAGGAATGCTGAGGGCCGC	795
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BM823479			
LOCUS			
DEFINITION			
5', mRNA sequence.			
ACCESSION			
BM823479			
VERSION			
EST.			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 622)			
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,			
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and			
Kim,Y.S.			
TITLE			
21C Frontier Korean EST Project 2001			
JOURNAL			
COMMENT			
Unpublished (2002)			
Contact: Kim YS			
Genome Research Center			
Korea Research Institute of Bioscience & Biotechnology			
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea			
Tel: +82-42-860-4470			
Fax: +82-42-860-4409			
Email: yongsung@mail.kribb.re.kr			
Plate: 102 row: H column: 01			
High quality sequence stop: 622.			
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/lab_host="DH10B"			
/clone_lib="S22SNU16n1"			
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Site 2: NotI; The S22SNU16 library was contributed by the			
Soares laboratory and it was constructed as described by			
Bonaldio, M.F., Lennon, G. and Soares, M.B. (1996), Genome			
Research 6(9): 791-806. RNA was prepared from harvested			
cells of SNU-16 culture. SNU-16 cell was obtained from			
Korean Cell Line Bank (KCLB). SNU-16 was established from			
ascitic fluids of Korean patients by Park J.G. et al.			
(1990), Cancer Res 50: 2773-2780."			
ORIGIN			
Query Match			
Best Local Similarity 100.0%; Pred. No. 1e-148;			
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	814	ACCAGTAAGATCTCGGACCTTATCAGCAGCATCACGAGGACTTACCACCTGGATGAGCAG	873
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QY	874	GATGTCGAGGGCGCGCTGGTACGCGCATCATTCGCACTTAGTACCCGAAGAGCCGTGCT	933
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QY	934	CGCCCAAGACCTCGAGGGTGGTTCAACTCGGGTGTGCCCCCAACCCGCTGTGCCCT	993
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QY	994	GACAGTGGCCATGAGACCATGCTGGGCTCAGCTCTCAGCAGGAGTGCAGTGCAG	1053
Db	181	GACAGTGGCCATGAGACCATGCTGGGCTCAGCTCTCAGCAGGAGTGCAGTGCAG	240
QY	1054	ATCTCCAGGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCTTATGAGCTCCA	1113
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QY	1114	GGGTACCCAGCAAGCCATGACTCATCTCTTCCAGGGACCGACACAGACTCTCGGGGCA	1173
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QY	1354	ATTTCACTGGGCGCATGATCTACATCTCTTGCATCCCAGCTGGTCTGATCCCTGCCA	1413
Db	541	ATTTCACTGGGCGCATGATCTACATCTCTTGCATCCCAGCTGGTCTGATCCCTGCCA	600
QY	1414	GGGCCCCCTTCCCTTCCTGCTCAT	1435
Db	601	GGGCCCCCTTCCCTTCCTGCTCAT	622
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DEFINITION			
582 bp mRNA linear EST 17-SBP-2004			
BP315176 Sugano cDNA library, mammary gland OCUB-F Homo sapiens			
CDNA clone OFR07979, mRNA sequence.			
ACCESSION			
BP315176			
VERSION			
BP315176.1 GI:52244151			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 582)			
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,			
Mizushima-Sugano,J., Nakai,K. and Sugano,S.			
TITLE			
Sequence comparison of human and mouse genes reveals a homologous			
block structure in the promoter regions			
JOURNAL			
Genome Res. 14 (9), 1711-1718 (2004)			
PUBMED			
15342556			
COMMENT			
Contact: Yutaka Suzuki			
Department of Virology			
Institute of Medical Science, University of Tokyo			
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan			
Email: yusukedi@ims.u-tokyo.ac.jp.			
FEATURES			
Location/Qualifiers			
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Query Match 33.7%; Score 577.8; DB 3; Length 582;
Best Local Similarity 99.7%; Pred. No. 2.5e-137;
Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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/notes="mammary gland tumor"

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Qy 520 TACCCGAGGCGCCTCCAGGCGCTGATGCGGACTCTGCTGCAAGGAGCCACTGGCC 579
Db 62 TACCCGAGGCGCCTCCAGGCGCTGATGCGGACTCTGCTGCAAGGAGCCACTGGCC 121
Qy 580 GATCCCCCACCACCTGCGACACAGCTCCGCCAGCAGCTTTGCCAGTAGTCTCTGTGGCTCC 639
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Qy 640 GAGGAGTACTATTCTTTCCATGAGTGGGACTGGGACTGGGAGATGGGAGTGGCTCC 699
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Qy 700 ATGTGAGCGGAGAAATTTGATGCTCATCTTCAAGAGCTGACAGAGCTGTTCAAGGTA 759
Db 242 ATGTGAGCGGAGAAATTTGATGCTCATCTTCAAGAGCTGACAGAGCTGTTCAAGGTA 301
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Db 302 CACCAGATCGATGAGTGGGCAAGTGCATCAGACACTGTGTTCTGGAGAGACCACT 361
Qy 820 AAGATCTCGGACCTTATCAGCAGCATCAAGCAGGACTACACCTGGATGAGCAGAGTGT 879
Db 362 AAGACCTCGGACCTTATCAGCAGCATCAAGCAGGACTACACCTGGATGAGCAGAGTGT 421
Qy 880 GAGGCGGCTGTGACGCGGATCATTCGATAGTACCCGAAAGAGCGGTGCTCGCCCA 939
Db 422 GAGGCGGCTGTGACGCGGATCATTCGATAGTACCCGAAAGAGCGGTGCTCGCCCA 481
Qy 940 CAGACCTCGGAGGCTGTTCAACTCGGGCTGCTGCCCAACCGCTGCTGCCCTGACAGT 999
Db 482 CAGACCTCGGAGGCTGTTCAACTCGGGCTGCTGCCCAACCGCTGCTGCCCTGACAGT 541
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RESULT 14
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603347838F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5375384 5',
mRNA sequence.
ACCESSION Bi694617
VERSION Bi694617.1 GI:15657246
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 826)
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-x@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1955 row: 1 column: 09
High quality sequence stop: 796.

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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 33.6%; Score 576.2; DB 3; Length 826;
Best Local Similarity 84.0%; Pred. No. 6.8e-137;
Matches 676; Conservative 0; Mismatches 123; Indels 6; Gaps 2;

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Db 61 GAAGGCTGTCCGAAGCCGCTGGGCCAAGGAAACAATGGTGTGCGCCCGAGCCCGGAC 120
Qy 418 CGTGACACCCCGGCGGGATGCGCGGCTCAAGTCAACCACTGGCAGCAGCTTC 477
Db 121 CGTGACACCCCGGCGGGATGCGCGGCTCAAGTCAACCACTGGCAGCAGCTTC 180
Qy 478 AGTACCCCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTACCGAGGGCCACTCC 537
Db 181 AGTACCCCTGATGTTAAGCTCAAGGATCCCTGTGTATCCCTACCGAGGGCCACTCC 240
Qy 538 CAGGCGGCTGATGCGGAGTCTGCTGCAAGGAGCAGTGGCCGATCCCCACCATCGCA 597
Db 241 CAGTCCCTGAGCGTGGACTCTGCTGCAAGGAGCAGTGGCCGAGCTCTCTCCACACG 300
Qy 598 CAGGCTGCCAGCAGCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
Db 301 CAGGCTGCCAGCAGCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 658 CATGAGTGGAGCCTGGAGCCTGGCGAGATGGGAGTGGGCTGCTGCTGCTGCTGCTGCT 717
Db 361 CATGAGTGGAGCCTGGAGCCTGGCTGAGTGGGAGTGGGCTGCTGCTGCTGCTGCTGCT 420
Qy 718 GATGCTCATCTTCAAGAGCTGACAGAGCTGTTTCAAGGTAACACAGATCGATGAGCTG 777
Db 421 GAGTGTCTTATTTTCAAGAGCTGACAGAGCTGTTTCAAGGTAACACAGATCGATGAGCTG 480
Qy 778 GCCAGTGCACATCAGACACTGTTCTTGGAGAGCAGTAAAGTCTCGGACCTTATC 837
Db 481 GCCAGTGCACATCAGACACTGTTCTTGGAGAGCAGTAAAGTCTCGGACCTTATC 540
Qy 838 AGCAGCATCAGCAGGACTACACCTGGATGAGCAGGATGCTGAGGCGGCGCTGGTACGC 897
Db 541 AGCAGCATCAGCAGGACTACACCTGGATGAGCAGGATGCTGAGGCGGCGCTGGTACGC 600
Qy 898 GGCATCATTTAGTAGTACCCGAAAGAGCGGTGCTGCGCCACAGACCTCGGAGGCTGT 957
Db 601 GGCATCATTTAGTAGTACCCGAAAGAGCGGTGCTGCGCCACAGACCTCGGAGGCGCG 660
Qy 958 TCACTCGGGCTGCGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGTG 1017
Db 661 TCACTCGGGCTGCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716

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Qy      1018 GGCTCAGGTCTCAGCCA--GGATGAGCTGAAGTGCAGATCTCCAGGACACGACTGCAG 1075
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       717 GGTCTGGCTCAGCCACGACGAACTGACAGTCAGATCTCCAGGAGACAACCGGA 776

Qy      1076 ATGCCATCGCCCGAAGCTGAGCC 1100
Db              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
       777 GATGCATCGCCAGGAACTGAAGGC 801


RESULT 15
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LOCUS   BP331524          583 bp    mRNA    linear    EST 17-SEP-2004
DEFINITION Sugano cDNA library, rectum Homo sapiens cDNA clone
RCT09504, mRNA sequence.
ACCESSION BP331524
VERSION   BP331524.1 GI:52260875
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shiokanadai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
     source           1..583
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="RCT09504"
                     /tissue_type="rectum"
                     /clone_lib="Sugano cDNA library, rectum"

ORIGIN
Query Match      31.5%; Score 540.2; DB 3; Length 583;
Best Local Similarity 98.3%; Pred. No. 1.2e-127;
Matches 575; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

Qy      19 CCGCGCCAGCATCTGGGCTCCACGCTTGAGACCGTGGAGCGGCCCAACAGACTTA-TG 77
Db              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
       1 CCGCGCCAGCATCTGGGCTCCACGCTTGAGACCGTGGAGCGGCCCAACAGAGCTATTG 60

Qy      78 TCTTGAGACATATGATAAACACCCTCAGCCCCCACCAAGCGCGCACCCCGTAGACCAGA 137
Db              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
       61 TCTTGAGACATATGATAAACACCCTCAGCCCCCACCAAGCGCGCACCCGTAGACCAGA 120

Qy      138 CCCCAAGGACCTGGCCACCAATGGCGCAGAGACATTACCTTCACTCTGGCTCTGCTGA 197
Db              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
       121 CCCCAAGGACCTGGCCACCAATGGCGCAGAGACATTACCTTCACTCTGGCTCTGCTGA 180

Qy      198 GCGGGCCCTTGAGTCCCACCTGCTGCCTGCTCTGGGACCCCTGGGTGTTGGAGTGGTG 257
Db              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
       181 GCGGGCCCTTGAGTCCCACCTGCTGCCTGCTCTGGGACCCCTGGGTGTTGGAGTGGTG 240

Qy      258 CCGGGCTGCCTTCTGCTTCCGCCGCTGCGGGATTGGCTCCAGCGCTGTGGAGCTCTGT 317
Db              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
       241 CCGGGCTGCCTTCTGCTTCCGCCGCTGCGGGATTGGCTCCAGCGCTGTGGAGCTCTGT 300

Qy      318 CGCGGGATGAGCCCTTGCCTGTCTTCTAGGACTCCACTGAGGGGACTGCTGAAGCAA 377
Db              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
       301 CGCGGGATGAGCCCTTGCCTGTCTTCTAGGACTCCACTGAGGGGACTGCTGAAGCAA 360

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Result No.	Score	Match	Quality %	Length	DB	ID	Description
1	1692.8	98.8	1785	3	US-10-104-047-799	Sequence 799, App	
C 2	46	2.7	4403765	3	US-09-103-840A-2	Sequence 2, Appl	
3	42.2	2.5	1767	3	US-09-016-434-1488	Sequence 1488, App	
C 4	41.4	2.4	2109	3	US-09-370-838-153	Sequence 153, App	
C 5	41.4	2.4	2109	3	US-09-854-133-153	Sequence 153, App	
C 6	40.8	2.4	438	3	US-09-489-039A-6029	Sequence 6029, Ap	
C 7	40.8	2.4	465	3	US-09-489-039A-6072	Sequence 6072, Ap	
8	40.8	2.4	930	3	US-09-489-039A-6078	Sequence 6078, Ap	
9	40.4	2.4	1503	3	US-09-797-039-3	Sequence 3, Appl	
10	40.4	2.4	2297	3	US-09-797-039-1	Sequence 1, Appl	
11	40.4	2.4	2747	3	US-09-620-312D-19	Sequence 19, Appl	
12	40.4	2.4	2840	3	US-09-620-312D-20	Sequence 20, Appl	
13	40.4	2.4	3124	3	US-09-734-030-1	Sequence 1, Appl	
14	40.4	2.4	3124	3	US-10-153-921-1	Sequence 1, Appl	
15	40.4	2.4	3124	3	US-10-669-689-1	Sequence 1, Appl	
16	40.2	2.3	975	3	US-09-902-540-9140	Sequence 9140, Ap	
17	40.2	2.3	10178	3	US-09-902-540-977	Sequence 977, App	
18	40.2	2.3	11935	3	US-09-949-016-1290	Sequence 14290, A	
19	40.2	2.3	11935	3	US-09-949-016-14291	Sequence 14291, A	
C 20	39.6	2.3	284	2	US-08-902-623-42	Sequence 42, Appl	
C 21	39.6	2.3	364	2	US-09-621-976-17202	Sequence 17202, A	
22	39.4	2.3	7218	2	US-08-232-463-14	Sequence 14, Appl	
23	39.2	2.3	430	3	US-09-621-976-16656	Sequence 16656, A	
24	39.2	2.3	1336	3	US-09-902-540-1945	Sequence 1945, Ap	

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QY 361 GGGACTGCTGAAGCCAACTGGGCGAAGGAGCAAAATGGAGTGCCCGCCAGCCCTGATCGT 420
Db 450 GGGACTGCTGAAGCCAACTGGGCGAAGGAGCAAAATGGAGTGCCCGCCAGCCCTGATCGT 509
QY 421 GCACCCCCCAGCGCGGGGATGGCCAGCGGCTCAAGTCAACCAATGGGCGAGCAGCTTCAGC 480
Db 510 GCACCCCCCAGCGCGGGGATGGCCAGCAGCTCAAGTCAACCAATGGGCGAGCAGCTTCAGC 569
QY 481 TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCAGGCGCCACCTCCCA 540
Db 570 TACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCAGGCGCCACCTCCCA 629
QY 541 GCCCTGTATGCGGACTTCCTGCTGAAGGAGCCACTGCGCCGATCCCGCCACCCATGGACAC 600
Db 630 GCCCTGTATGCGGACTTCCTGCTGAAGGAGCCACTGCGCCGATCCCGCCACCCATGGACAC 689
QY 601 AGCCTGCCAGCACCTTTGCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTCTTTCCAT 660
Db 690 AGCCTGCCAGCACCTTTGCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTCTTTCCAT 749
QY 661 GAGTCGGACCTTGACCTGCGCGAGATGGGAGTGGGCTCCATGTCGAGCGGAGAAATGAT 720
Db 750 GAGTCGGACCTTGACCTGCGCGAGATGGGAGTGGGCTCCATGTCGAGCGGAGAAATGAT 809
QY 721 GTGCTCATCTTCAAGAAGCTGCAGAGCTGTTCAAGGTACACAGATCGATGAGCTGGCC 780
Db 810 GTGCTCATCTTCAAGAAGCTGCAGAGCTGTTCAAGGTACACAGATCGATGAGCTGGCC 869
QY 781 AAGTGCAATCAGACACTGTGTTCTCTGGAGAACACCAAGTAAAGTCTCGGACCTTATCAGC 840
Db 870 AAGTGCAATCAGACACTGTGTTCTCTGGAGAACACCAAGTAAAGTCTCGGACCTTATCAGC 929
QY 841 AGCATCAGCGAGACTACCACTGTGATGAGCAGGATGCTGAGGCGCGCCTGTGTAACGCGC 900
Db 930 AGCATCAGCGAGACTACCACTGTGATGAGCAGGATGCTGAGGCGCGCCTGTGTAACGCGC 989
QY 901 ATCATTTCGATAGTACCGAAGAGCCGTGCTCGCCACAGACCTCGGAGGGTCTGTCA 960
Db 990 ATCATTTCGATAGTACCGAAGAGCCGTGCTCGCCACAGACCTCGGAGGGTCTGTCA 1049
QY 961 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGC 1020
Db 1050 ACTCGGGCTGCTGCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGC 1109
QY 1021 TCAGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGAGACGACTGCAGATGCC 1080
Db 1110 TCAGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGAGACGACTGCAGATGCC 1169
QY 1081 ATGCCCCGAGCTGAGGCTTATGAGCTCCAGGGTACCCAGACCATGACTCATCC 1140
Db 1170 ATGCCCCGAGCTGAGGCTTATGAGCTCCAGGGTACCCAGACCATGACTCATCC 1229
QY 1141 TTCAGGCGACCGACAGACTCGTCGGGGGACCCCTGCTCCAGGTGACTGCTAAACC 1200
Db 1230 TTCAGGCGACCGACAGACTCGTCGGGGGACCCCTGCTCCAGGTGACTGCTGACCC 1289
QY 1201 CTGCGCAGGCCCCAGCTGCCACACCCCTTTCTGGGAGAGCATGGCCCTACAGAAAGAGGG 1260
Db 1290 CTGCGCAGGCCCCAGCTGCCACACCCCTTTCTGGGAGAGCATGGCCCTACAGAAAGAGGG 1349
QY 1261 GGNACAGGAACCCCTGTGGGAGGCTTAGACCTGAAGCAGTCCCACTCTGGCTCTCC 1320
Db 1350 GGNACAGGAACCCCTGTGGGAGGCTTAGACCTGAAGCAGTCCCACTCTGGCTCTCC 1409
QY 1321 TGCCTTTGGCTGACTGGGTCTCTGGACCATGTGATTTCACTGGGCCATGGGATCTACATC 1380
Db 1410 TGCCTTTGGCTGACTGGGTCTCTGGACCATGTGATTTCACTGGGCCATGGGATCTACATC 1469
QY 1381 TCCTTCATCCCGACTGCTGATCCCTGCGCAGGCGCCCTTCCTTCTGCTCATGGTCT 1440
Db 1470 TCCTTCATCCCGACTGCTGATCCCTGCGCAGGCGCCCTTCCTTCTGCTCATGGTCT 1529
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QY 1441 TCAGTGGCGCTGATCATGGAAGTAAGGAGTTAGGCATTACCTTCTGGAGTGAAACCCTG 1500
Db 1530 TCAGTGGCGCTGATCATGGAAGTAAGGAGTTAGGCATTACCTTCTGGAGTGAAACCCTG 1589
QY 1501 ACTCATCCCCCTATTTGCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT 1560
Db 1590 ACTCATCCCCCTATTTGCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT 1649
QY 1561 TCAACAGTTTAAAGAGCTTATCTTAAATGATTTGTTGGGGGTGGGCAGGGCCCACT 1620
Db 1650 TCAACAGTTTAAAGAGCTTATCTTAAATGATTTGTTGGGGGTGGGCAGGGCCCACT 1709
QY 1621 CTATGTTATGTTAAGGAGTTGTTCTTGGTCTTGGCTGATGTTCTGTATCTTAAACATGAC 1680
Db 1710 CTATGTTATGTTAAGGAGTTGTTCTTGGTCTTGGCTGATGTTCTGTATCTTAAACATGAC 1769
QY 1681 CACAGTTTGTAAAGTAC 1696
Db 1770 CACAGTTTGTAAAGTAC 1785
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RESULT 2
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen K.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: TUBERCULOSIS
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 2.7%; Score 46; DB 3; Length 4403765;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 115; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 108 CCCACCAAGCCGCGCACCCGTAGACCAAGGACCCCTGGCCACCATGGGCCAGA 167
Db 3929345 CCGCGCCCGCCGCTTCGCGCCGCTCCCAACGCTTGGCCGCGCGCCGCC 3929286

QY 168 GAGCATTAATCTTCATCTGCTCTGAGCGCGCCCTTGGTCCCGCTGCTGCT 227
Db 3929285 TCGCTCGCCACGCTGCTTCGTTCTGCGCTACACCGCCCGCGCGCTGCGCG 3929226

QY 228 GCTCTGGCGACCTTGGGTGTGGGAGTGTGCGCGGCTGCTTCTGCTCCGCGCTGCCG 287
Db 3929225 GTGCCCGCGCCCGCTTGTATGCGCGCGCGCGCGCTTGGCGCGCCCGCTTGGCG 3929166

QY 288 GGAATGCTTCAGCGCTGTGGAGCCCTGTGTGGGGATGAGACCCCTGCC 337
Db 3929165 CTTGGCCCGCGCGAAGCCGTTGCGCTTCTTGGGAGAGGCGCGCGCTGTC 3929116

RESULT 3
US-09-016-434-1488
; Sequence 1488, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:

APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1488:
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
LIBRARY: GENBANK
CLONE: 995934
US-09-016-434-1488

Query Match 2.5%; Score 42.2; DB 3; Length 1767;
Best Local Similarity 48.3%; Pred. No. 0.42;
Matches 215; Conservative 0; Mismatches 218; Indels 12; Gaps 3;
Qy 2 TGGCCCGCCCTGGACACCCCGCCGACATCTGGGCTCCACGCTTGGGACCGTGGGAGC 61
Db 199 TGACACGCTGTGGCCCGCCCGCCCTTCCCGGTCTGGGCTGGGACTCCCGGG---GGGTGGGC 255
Qy 62 GGCCAAACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCGCCCAACCAAGCGCC 121
Db 256 GGCTCATGNACTCTTCCCGCCACCTCAGGCTCAGCCAGAACCCCTCGAGTGGG 315
Qy 122 GCACCGGTAGACAGACCCCAAGAGACCTGGCCACCATGGGCGAGAGATTACTTCA 181
Db 316 GCTGAGCTCAGTCCCGCTTCTTGGCTCCAGGGCTGCGCCAGAGTCCATTCCAGGCC 375
Qy 182 TCTCTGGCTGTGAGCGCGCCCTTGAGTCCCGCCACCTGCTGCTGCTTGGGACCT 241
Db 376 GCGCCGCGCGCCCGCCCGCCAGCCCGCCCGCGCGCGCGCTTCCAGGTGGACTTG 435
Qy 242 GGGTGTGGAGTGGTGGCGGGCTGCTTCTGCTTCCGCGCGCTGCGGGATTGCTCCAGC 301
Db 436 CTCCCGGTGTCCCGCGCGCCAGAGTCCCGCGGGCTGCTGGCGCGCTGCGCGCT 495
Qy 302 GCTGTGAGCTGTGTGCGGGATGACGCCCTTGGCTG---TCTACTGAGGACTC--- 353
Db 496 GCTGCGCGCGCTGCTGCGCGCGCCCGCGCGCGCTTCTACGGTGGACACAGCG 555
Qy 354 -CACTGAGGGAGTGTGAGGCCAACTGGGCGAGGAGCATGAGTGGTCCCCCGCCAGCC 412

Db 556 GCCTGNAAGCAGCCTCGGCGCGCCCTCCCGACCCCGCCAGTGTGCGCGCCCGCGGCC 615
Qy 413 CTGATGTGCACCCCGCCAGCGCGC 437
Db 616 GAGCGCGCGCCCGCCCGCTCGCGC 640
RESULT 4
US-09-370-838-153/c
; Sequence 153, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 153
; LENGTH: 2109
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-153

Query Match 2.4%; Score 41.4; DB 3; Length 2109;
Best Local Similarity 46.9%; Pred. No. 0.74;
Matches 129; Conservative 0; Mismatches 146; Indels 0; Gaps 0;
Qy 179 TCATCTCTGGCTCTGTGAGCGCGCCCTTGAGTCCCGCCACCTGCTGCTCTCTGGCGAC 238
Db 764 TCTCCCGCGCGCCCTGCTGTCTGGGCGCCCGGGCTCTCCCTGGGGCCACCTCGCGCTG 705
Qy 239 CTTGGGTGTGGAGTGTGCGCGGCTGCTTCTGCTTCCCGCGCTGCGGGATTGCGCTCC 298
Db 704 GCTCTCGGGCGCGCTGGCTCCAGCCTCTCGGCTGTGCTCCGCTGGCGTGGCAGCGGT 645
Qy 299 AGCGCTGTGAGCCTGTGTGCGGGGATGACGCCCTGCTCTACTGAGACTCTCACTG 358
Db 644 GCGCGCGGTGGTGTGCGGCTCTGTTGTCTACCCATCCGCGCTTGGGTCCAGCGCGCTT 585
Qy 359 AGGGGACTCTGAAGCAACTGGGCGCAAGAGACCAATGAGTGGCCCCCGCCAGCTGATC 418
Db 584 CCGGGCGCGCGCGCGCGGGCGCTCCCGCTGCGCCACTGGGGCTCGGGCCCCCACCCTCCGAGG 525
Qy 419 GTGCACCCCGCCAGCGCGCGGATGGCAGCGGCTC 453
Db 524 TCCAGCTCCAGCGCCCTGGGGCTCTGGGCGCCCC 490

RESULT 5
US-09-854-133-153/c
; Sequence 153, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 153
; LENGTH: 2109
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-153

Query Match      2.4%; Score 41.4; DB 3; Length 2109;
Best Local Similarity 46.9%; Pred. No. 0.74;
Matches 129; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

QY 179 TCATCTCTGGCTCTGTGTAGACGGCCCTTTAGTCCCCACCTGCTGCTCTGTGGCGAC 238
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
764 TCTCGCCGGCCTGTGTCTGGGGCCCGGGCTCTCCCTCGGGGCCACCTCGGGCCTG 705
QY 239 CTGGGTGTGGAGTGTGTCGGGCTGCTTCTGTCTCCGCCGCTGCCGGATTGCTCC 298
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
704 GTCTCTGGGGGGCTGGCTCCAGCCTCTCTCGGTGTGCTTCCGGTGGCGGTGGCAGCGT 645
QY 299 AGCGCTGTGGAGCCTGTGTGCGGGATGAGCCCTGCTCTACTGAGGACTCCACTG 358
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
644 GCGGGCGTGGTGGCCCTCTGTGTGTCTACCATCCGGCCTTTGCTCCAGCGCTT 585
QY 359 AGGGACTCTGAAGCAACTGGGCAAGAGACAAATGAGTGGCCCCCAGCCTTGATC 418
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
584 CCGGGCCCGCCGGGGGCGCTGCCGTGCCACTTGGGGCTCGGGCCCACTCCCGAGG 525
QY 419 GTGCACCCCGGCGGGGATGGCCAGGGCTC 453
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
524 TCAGCCTCCAGCCCTCGGGGCTCTCGGGGCCCC 490

RESULT 6
US-09-489-039A-6029
; Sequence 6029, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6029
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6029

Query Match      2.4%; Score 40.8; DB 3; Length 438;
Best Local Similarity 48.6%; Pred. No. 0.55;
Matches 140; Conservative 0; Mismatches 147; Indels 1; Gaps 1;

QY 6 CCGCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCTGGGAGCGGC 65
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
144 CGCGCTCGGCTCGATGCTGACGGTGACAGCGCCGGCGGACCGTCTATCTATC 203
QY 66 AACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGCGCGCAC 125
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
204 TCGCGGCCCGGATCTCGGGCGGACGCTCGCGACAGAGTCCGCGCACCTCGCGCCA 263
QY 126 CGGTAGACAGACCCCAAGACCTTGCCTGAGTCCCGCCACCATGGCCAGAGATTACCTTATCTC 185
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
264 GCGGCTCGGCTCGATGCTGCTGCTGATCGGCGACGCTCTCTTCTTGGGCG 205
QY 186 TGGCTCTGTAGCGCGCCCTTGTAGTCCCGCCACCTGCTGCTGTGCGGACCTGGGT 245
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
324 TAGAGCGCAGGGGTGCGGTTGA-TCCGCGCCCTGCTGCTTATCTGAGACGCTGGGT 382
QY 246 GTGGGAGTGTGCGGGCTCTTGTCTTCCGCGCTCGCGGATTG 293
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 383 ATCGCCTGGCGCGGTGTGTGTCGCGCATCAGTCGCGGTGGCGCTG 430

RESULT 7
US-09-489-039A-6072/c
; Sequence 6072, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6072
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6072

Query Match      2.4%; Score 40.8; DB 3; Length 465;
Best Local Similarity 48.6%; Pred. No. 0.56;
Matches 140; Conservative 0; Mismatches 147; Indels 1; Gaps 1;

QY 6 CCGCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCTGGGAGCGGC 65
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
384 CGCGCTCGGCTCGATGCTGCTGCTGATCGGCGACGCTCTGCTGATCGGCGACGCTCTCTTCTTGGGCG 205
QY 66 AACAGAGCTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGCGCGCAC 125
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
324 TCGCGGCCCGGATCTCGGGCGGACGCTCGCGACAGAGTCCGCGCACCTCGCGCCA 265
QY 126 CGGTAGACAGACCCCAAGACCTTGGCCACCATGGCCAGAGATTACCTTATCTC 185
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
264 GCGGCTCGGCTCGGCGCCGACGCTGCTGCTGATCGGCGACGCTCTCTTCTTGGGCG 205
QY 186 TGGCTCTGTAGCGCGCCCTTGTAGTCCCGCCACCTGCTGCTGTGCGGACCTGGGT 245
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
204 TAGAGCGCAGGGGTGCGGTTGA-TCCGCGCCCTGCTGCTTATCTGAGACGCTGGGT 146
QY 246 GTGGGAGTGTGCGGGCTCTTGTCTTCCGCGCTCGCGGATTG 293
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-09-489-039A-6078
; Sequence 6078, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6078
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6078

Query Match      2.4%; Score 40.8; DB 3; Length 930;
Best Local Similarity 48.6%; Pred. No. 0.76;
Matches 140; Conservative 0; Mismatches 147; Indels 1; Gaps 1;

QY 6 CCGCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACCTGGGAGCGGC 65
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Db 332 CGGCGCTCGGCTCGATGCTCCCTGACGGTGCACAGCGCCGCGGACCGTCATACCTATC 391
Qy 66 AACAGAGCTATGTCTGGAGACATATGATAAACACCACTTCAGCCCCCAAGCGCGCGCAC 125
Db 392 TGGCGGCGCGGATCTCGGGGGGAGCTCGCCGACGAGATCGGCGGACCTCGCGGCA 451
Qy 126 CCGTAGACAGACCCCAAGACCCCTGGCCACCAATAGGCGCCAGAGAGANTTACCTTCATC 185
Db 452 GCGGCGTCCGCGCGGCGGACCTGCTGTGTGTGATCGGCGGCGGCTCTCTTCCTGGGCGG 511
Qy 186 TGCTCTGCTGAGCGCGGCGCTGAGTCCCGCCCACTGCTGCTGCTGCGGACCCCTGGGT 245
Db 512 TAGAGCGCCAGGGGTGCCGTGGA-TCCGCGCCCTGCTGCCCTATCTGCAGAGCTGGGT 570
Qy 246 GTGGGAGTGTGCGGCGCTGCCCTTCTGCTTCGCGCGCTGCGGAGATG 293
Db 571 ATCGGCTGAGCGCGGTGGTGGTCTGCGGCATCAGTCGCGGGTGGCGTG 618

RESULT 9
US-09-797-039-3
; Sequence 3, Application US/09797039
; Patent No. 6730491
; GENERAL INFORMATION:
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
; TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
; FILE REFERENCE: 10448-017001
; CURRENT APPLICATION NUMBER: US/09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-797-039-3

Query Match 2.4%; Score 40.4; DB 3; Length 1503;
Best Local Similarity 53.9%; Pred. No. 1.2;
Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 713 AAATTGATGTGCTCATCTTCAAGAAGCTGCAGAGCTGTTTCAGGTACACCATCGATG 772
Db 203 AGAACGAGATAGGCATCTCAAGATGGTGAAGCATCCAAACATCTCTACAGCTGGTGATG 262
Qy 773 AGCTGGCCAAAGTGCATCAGACACTGTGTTCTCTGGAGAGACAGTAAGATCTCGGACC 832
Db 263 TGTGTTGACCCGACAGGAGTACTTTATCTTCTGAGCTGGCCACGGGAGGAGGTGT 322
Qy 833 TTATCAGCAGCATCAGCAGGACTTACCACTCGA 866
Db 323 TTGACTGGATCTGGACAGGAGGCTACTACTCGGA 356

RESULT 10
US-09-797-039-1
; Sequence 1, Application US/09797039
; Patent No. 6730491
; GENERAL INFORMATION:
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
; TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
; FILE REFERENCE: 10448-017001
; CURRENT APPLICATION NUMBER: US/09/797,039
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1656)
; NAME/KEY: misc feature
; LOCATION: (1)...(2297)
; OTHER INFORMATION: n = A,T,C or G
US-09-797-039-1

Query Match 2.4%; Score 40.4; DB 3; Length 2297;
Best Local Similarity 53.9%; Pred. No. 1.4;
Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 713 AAATTGATGTGCTCATCTTCAAGAAGCTGCAGAGCTGTTTCAGGTACACCATCGATG 772
Db 356 AGAACGAGATAGGCATCTCAAGATGGTGAAGCATCCAAACATCTCTACAGCTGGTGATG 415
Qy 773 AGCTGGCCAAAGTGCATCAGACACTGTGTTCTCTGGAGAGACAGTAAGATCTCGGACC 832
Db 416 TGTGTTGACCCGACAGGAGTACTTTATCTTCTGAGCTGGCCACGGGAGGAGGTGT 475
Qy 833 TTATCAGCAGCATCAGCAGGACTTACCACTCGA 866
Db 476 TTGACTGGATCTGGACAGGAGGCTACTACTCGGA 509

RESULT 11
US-09-620-312D-19
; Sequence 19, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 658662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 19
; LENGTH: 2747
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)..(1618)
US-09-620-312D-19
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Matches	83;	Conservative	0;	Mismatches	71;	Indels	0;	Gaps	0;
Qy	713	AAATTGATGTCTCATCTTCAAGAAGCTGACAGAGCTGTTTCAGCGTACACCGATCGATG	772						
Db	413	AGAACGAGATAGGCATCTCAAGATGTGAAGCATCCCAACATCTCTACAGCTGCTGGATG	472						
Qy	773	AGCTGGCCAAAGTGACATCATGACACTGTGTTCTTGGAGAAAGACAGTAAAGATCTCGGACC	832						
Db	473	TGTTTGTCGCCGCAAGGAGTACTTTTATCTTCTGGAGCTGGCCACGGGAGGGAGGTGT	532						
Qy	833	TTATCAGCAGCATCACCGAGCTACACCTGGA	866						
Db	533	TTGACTGGATCCTGGACCGAGGGTACTACTCGGA	566						

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RESULT 15
US-10-669-689-1
; Sequence 1, Application US/10669689
; Patent No. 6800471
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000612DIVII
; CURRENT APPLICATION NUMBER: US/10/669,689
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 09/734,030
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/207,281
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3124
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-689-1

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	Query Match	2.4%	Score 40.4	DB 3	Length 3124
	Best Local Similarity	53.9%	Pred. No. 1.6		
	Matches	83	Conservative	0	Mismatches 71; Indels 0; Gaps 0;
Qy	713	AAATTGATGCTCATCTTCCAAGAGCTGACAGAGCTGTTTCAGGGTACACCATGATCGATG	772		
Db	413	AGAACGAGATAGGCATCCTCAAGATGGTGAAGCATCCCAATCCTACAGCTGGTGGATG	472		
Qy	773	AGCTGGCCAAAGTGACATCAGACACTGTGTTCTCTGGAGAAAGACAGTAAAGATCTCGGACC	832		
Db	473	TGTTTGTGACCCGCAAGGAGTACTTTTATCTTCTGGAGCTGGCCACGGGAGGGAGGTGT	532		
Qy	833	TTATCAGCAGCATCACGACGACTTACCACCTGGA	866		
Db	533	TTGACTTGGATCTCTGGACACGGGGTACTACTTCGGA	566		

Search completed: March 11, 2006, 20:06:17
Job time : 329 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1713	100.0	1713	3	US-09-989-890-105	Sequence 105, App
2	1692.8	98.8	1785	6	US-10-104-047-799	Sequence 799, App
3	1602.4	93.5	1977	3	US-09-989-920-56	Sequence 56, App1
4	1602.4	93.5	1977	3	US-09-989-920-117	Sequence 117, App
5	607.6	35.5	654	5	US-10-074-475-124	Sequence 124, App
6	463.2	27.0	728	9	US-10-779-543-5731	Sequence 5731, Ap
7	385	22.5	385	3	US-09-989-920-55	Sequence 55, App1
8	380.2	22.2	386	3	US-09-989-890-104	Sequence 104, App
9	380.2	22.2	386	5	US-10-074-475-123	Sequence 123, App
10	352.6	20.6	393	9	US-10-779-543-10096	Sequence 10096, A
11	347	20.3	427	9	US-10-779-543-12051	Sequence 12051, A
12	300	17.5	300	9	US-10-779-543-1705	Sequence 1705, Ap
13	298.4	17.4	300	5	US-10-076-555-34	Sequence 34, App1
14	298.4	17.4	300	9	US-10-779-543-30	Sequence 34, App1
15	120	7.0	120	3	US-09-989-920-116	Sequence 116, App
16	46.4	2.7	2761	6	US-10-094-749-973	Sequence 973, App
17	45.6	2.7	513	6	US-10-029-386-10967	Sequence 10967, A
18	45.6	2.7	1242	7	US-10-437-963-6792	Sequence 6792, Ap
19	43	2.5	2359	5	US-10-091-438-44	Sequence 44, App1
20	43	2.5	2359	3	US-09-764-853-144	Sequence 144, App
21	42.8	2.5	2370	7	US-10-425-114-16503	Sequence 16503, A
22	42.2	2.5	1767	6	US-10-305-720-1488	Sequence 1488, Ap
23	42.2	2.5	1767	8	US-10-723-860-3497	Sequence 3497, Ap

Db 241 TGGGTGTGGAGTGTGTCGGGCTGCTTCTGCTTCGCGCGCTGCGGGATGTCCTCCAG 300
QY 301 CGCTGTGAGACTGTGTGCGGGATGACAGCCCTGCTGTCTACTAGAGACTCCACTGAG 360
Db 301 CGCTGTGAGACTGTGTGCGGGATGACAGCCCTGCTGTCTACTAGAGACTCCACTGAG 360
QY 361 GGGACTGCTGAAGCAACTGGGCAAGGAGACAAATGGAGTGCCCCCAGCCCTGATCGT 420
Db 361 GGGACTGCTGAAGCAACTGGGCAAGGAGACAAATGGAGTGCCCCCAGCCCTGATCGT 420
QY 421 GCACCCCCCAGCGGGGATGCCAGCGGCTCAAGTCAACCATGGGACAGACTTCAGC 480
Db 421 GCACCCCCCAGCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGACAGACTTCAGC 480
QY 481 TACCCCGATGTTAAGCTCAAAAGCATCCCTGTGTATCCCTACCCGAGGGCCACTCCCA 540
Db 481 TACCCCGATGTTAAGCTCAAAAGCATCCCTGTGTATCCCTACCCGAGGGCCACTCCCA 540
QY 541 GCCCTGTATGCGGACTCTGCTGCAAGGAGCCACTGGCCGATCCCCCAGCCATGGACAC 600
Db 541 GCCCTGTATGCGGACTCTGCTGCAAGGAGCCACTGGCCGATCCCCCAGCCATGGACAC 600
QY 601 AGCCTGCCAGCACCCTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTCCAT 660
Db 601 AGCCTGCCAGCACCCTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTCCAT 660
QY 661 GAGTGGGACTGTGACCTGCGGAGATGGGAGTGGCTCCATGTGAGCGGAGAAATGTAT 720
Db 661 GAGTGGGACTGTGACCTGCGGAGATGGGAGTGGCTCCATGTGAGCGGAGAAATGTAT 720
QY 721 GTGCTCATCTCAAGAGCTGACAGAGCTGTTTCAGCGTACACAGATCATGAGCTGGCC 780
Db 721 GTGCTCATCTCAAGAGCTGACAGAGCTGTTTCAGCGTACACAGATCATGAGCTGGCC 780
QY 781 AAGTGACATCAGACACTGTGTTCTCGGAGAGACCAAGTAAAGATCTCGGACCTTATCAGC 840
Db 781 AAGTGACATCAGACACTGTGTTCTCGGAGAGACCAAGTAAAGATCTCGGACCTTATCAGC 840
QY 841 AGATCACCGAGACTACCACTGGATGAGAGGATGCTGAGGGCGGCTGTGATGCGGCG 900
Db 841 AGCATCACCGAGACTACCACTGGATGAGAGGATGCTGAGGGCGGCTGTGATGCGGCG 900
QY 901 ATCATTCGCAATAGTACCCGAAAGACCGTGTGCTCGCCCAACAGACTCGGAGGGTGTTC 960
Db 901 ATCATTCGCAATAGTACCCGAAAGACCGTGTGCTCGCCCAACAGACTCGGAGGGTGTTC 960
QY 961 ACTCGGGCTGCTGCCCAACCGCTGTGCCCCCTGACAGTGGCCATGAGACCATGCTGGGC 1020
Db 961 ACTCGGGCTGCTGCCCAACCGCTGTGCCCCCTGACAGTGGCCATGAGACCATGCTGGGC 1020
QY 1021 TCAGTGTCTCAGCAGGATGAGTGAAGTGTGAGATCTCCAGAGACGATGAGATGCC 1080
Db 1021 TCAGTGTCTCAGCAGGATGAGTGAAGTGTGAGATCTCCAGAGACGATGAGATGCC 1080
QY 1081 ATGCCCCGAAGCTGAGGCTTATGAGCTCAGGGTACCCAGAGCCATGACTCATCC 1140
Db 1081 ATGCCCCGAAGCTGAGGCTTATGAGCTCAGGGTACCCAGAGCCATGACTCATCC 1140
QY 1141 TTCCAGGGGACCGACACAGACTCGTGGGGGACCCCTTGTCTCAGGTGTACTGCTAAACCC 1200
Db 1141 TTCCAGGGGACCGACACAGACTCGTGGGGGACCCCTTGTCTCAGGTGTACTGCTAAACCC 1200
QY 1201 CTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGCGCTACAGATGAGAGGG 1260
Db 1201 CTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAGCATGCGCTACAGATGAGAGGG 1260
QY 1261 GGACCAAGGAAACCCCTGTGGGAGAGGCTTAGACTGAAGCAGTCCCACTCTGGCTCTCC 1320
Db 1261 GGACCAAGGAAACCCCTGTGGGAGAGGCTTAGACTGAAGCAGTCCCACTCTGGCTCTCC 1320
QY 1321 TGCCTTGGCTGACTGGGTTCTTGAGACCATGTGATTTCACTGGGCCATGGGATCTACATC 1380

Db 1321 TGCCTTGGCTGACTGGGTTCTCTGGACCATGTGATTTCACTGGGCCATGGGATCTACATC 1380
QY 1381 TGCCTTGCATCCCACTGGTCTGATCCCTGCGAGGGCCCTTCCCTTCCTGCTCATGGTCT 1440
Db 1381 TGCCTTGCATCCCACTGGTCTGATCCCTGCGAGGGCCCTTCCCTTCCTGCTCATGGTCT 1440
QY 1441 TCAGTGGGCTGATCATGGAAGTAAAGGAGTTAGGCATTACCTTCTGGGAGTGAAACCTTG 1500
Db 1441 TCAGTGGGCTGATCATGGAAGTAAAGGAGTTAGGCATTACCTTCTGGGAGTGAAACCTTG 1500
QY 1501 ACTCCATCCCCCTATTGGCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGTAAT 1560
Db 1501 ACTCCATCCCCCTATTGGCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGTAAT 1560
QY 1561 TCAACAGTTAAAGAGCTTATCTTAAATGTATTGTATTGGGGGTGGGACGGGCCACT 1620
Db 1561 TCAACAGTTAAAGAGCTTATCTTAAATGTATTGTATTGGGGGTGGGACGGGCCACT 1620
QY 1621 CTATGTTATGTTAAGAGTGGTCTCTGGTTCCTGGCTGATGTTCTGTATCTTTAAATGAC 1680
Db 1621 CTATGTTATGTTAAGAGTGGTCTCTGGTTCCTGGTTCCTGGTTCCTGTGATGTTCTGATCTTAAATGAC 1680
QY 1681 CACAGTTTGTAAAGTACCTCGGCCGACACGC 1713
Db 1681 CACAGTTTGTAAAGTACCTCGGCCGACACGC 1713

RESULT 2
US-10-104-047-799
; Sequence 799, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 799
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-799

Query Match 98.8%; Score 1692.8; DB 6; Length 1785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACGCTGGGAG 60
Db 90 ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGGACGCTGGGAG 149
QY 61 CGGCCAACAGAGCTATGCTGGAGACATATGATAAACACCTCAGCCGCCACCAAGCCGC 120
Db 150 CGGCCAACAGAGCTATGCTGGAGACATATGATAAACACCTCAGCCGCCACCAAGCCGC 209
QY 121 CGCACCCGTAGACACGACCCCAAGGACCCCTGGCCACCATGGGCCAGAGAGCATTTACCTTC 180
Db 210 CGCACCCGTAGACACGACCCCAAGGACCCCTGGCCACCATGGGCCAGAGAGCATTTACCTTC 269
QY 181 ATCTCTGGCTCTGCTGAGCGGCGCTTGTAGTCCGCCACCTGCTGCTGCTGGCGACCC 240
Db 270 ATCTCTGGCTCTGCTGAGCGGCGCTTGTAGTCCGCCACCTGCTGCTGCTGGCGACCC 329
QY 241 TCGGTTGGGAGTGGTGGCGGCTGCTCTCTCCGCGCTGCGCGGATTCGCTCCAG 300
Db 330 TCGGTTGGGAGTGGTGGCGGCTGCTCTCTCCGCGCTGCGCGGATTCGCTCCAG 389
QY 301 CGCTGTGGAGCCTGTGTGCGGGATGACAGCCCTGCTCTACTGAGAGCTCCACTGAG 360

Db 390 CGCTGTGGAGCCTGTGTGCGGGGATGCAGCCCTTGCCTGTCTACTGAGGACTCCACTGAG 449
Qy 361 GGGACTGCTCAAGCCAACTGGGCGCAGAGACAATAGGAGTGGCCCGCCAGCCCTGTATCGT 420
Db 450 GGGACTGCTCAAGCCAACTGGGCGCAGAGACAATAGGAGTGGCCCGCCAGCCCTGTATCGT 509
Qy 421 GCACCCCGCAGCGCGGGATGSCCAGCGGCTCAAGTCAACCATGGCAGCAGCTTCAGC 480
Db 510 GCACCCCGCAGCGCGGGATGSCCAGCAGCTCAAGTCAACCATGGCAGCAGCTTCAGC 569
Qy 481 TACCCCGATTTAAGCTCAAGGCGATCCCTGTGTATCCCTACCCGAGGGCCACTTCCCCA 540
Db 570 TACCCCGATTTAAGCTCAAGGCGATCCCTGTGTATCCCTACCCGAGGGCCACTTCCCCA 629
Qy 541 GCCCTGATCGGAGCTCTCTGTCGAGAGGACCACTGSCCGATCCCCACCCCATGCGACAC 600
Db 630 GCCCTGATCGGAGCTCTCTGTCGAGAGGACCACTGSCCGATCCCCACCCCATGCGACAC 689
Qy 601 AGCCTGCCAGACACTTTGCGAGTGTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 690 AGCCTGCCAGACACTTTGCGAGTGTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 749
Qy 661 GAGTCGGACCTGGACCTTGCAGAGATGGGCACTGGCTCCATGTCGAGCCGAGAAATTGAT 720
Db 750 GAGTCGGACCTGGACCTTGCAGAGATGGGCACTGGCTCCATGTCGAGCCGAGAAATTGAT 809
Qy 721 GTCTCATCTTCAAGAACTGACAGAGCTGTTCAAGGTCACACAGATCGATGAGCTGGCC 780
Db 810 GTCTCATCTTCAAGAACTGACAGAGCTGTTCAAGGTCACACAGATCGATGAGCTGGCC 869
Qy 781 AAGTCACATCAGACACTGTTCTTCTGAGAGACCAAGTAAAGTCTCGGACCTTATCAGC 840
Db 870 AAGTCACATCAGACACTGTTCTTCTGAGAGACCAAGTAAAGTCTCGGACCTTATCAGC 929
Qy 841 AGCATCAGCAGGACTACCACTGGATGAGCAGGCTGCTGAGGGCGGCTGTTGACGGGC 900
Db 930 AGCATCAGCAGGACTACCACTGGATGAGCAGGCTGCTGAGGGCGGCTGTTGACGGGC 989
Qy 901 ATCAATTCGATTAAGTACCCGAAAGACCGTGTCTGCGCCACAGACCTCGGAGGTCGTTCA 960
Db 990 ATCAATTCGATTAAGTACCCGAAAGACCGTGTCTGCGCCACAGACCTCGGAGGTCGTTCA 1049
Qy 961 ACTCGGGCTGCTGCCCCAAGCGTGTGCCCCCTGACAGTGGCCATGAGACCATGTTGGCC 1020
Db 1050 ACTCGGGCTGCTGCCCCAAGCGTGTGCCCCCTGACAGTGGCCATGAGACCATGTTGGCC 1109
Qy 1021 TCAGGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGACGACTGCAGATGCC 1080
Db 1110 TCAGGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGACGACTGCAGATGCC 1169
Qy 1081 ATGCCCCGGAAGCTGAGGCTTATGAGGCTTCCAGGCTACCCAGAACCCATGACTCATCC 1140
Db 1170 ATGCCCCGGAAGCTGAGGCTTATGAGGCTTCCAGGCTACCCAGAACCCATGACTCATCC 1229
Qy 1141 TTCAGGGCACCGACACAGACTGTCGCGGGGCAACCTTGTCTCAGGTGACTGCTAAACC 1200
Db 1230 TTCAGGGCACCGACACAGACTGTCGCGGGGCAACCTTGTCTCAGGTGACTGCTGACCC 1289
Qy 1201 CTGCGAGGCCAGCTGCCACACCTTTCTGGGAGAGAGCTGCGCTACAGATGCAAGAGGG 1260
Db 1290 CTGCGAGGCCAGCTGCCACACCTTTCTGGGAGAGAGCTGCGCTACAGATGCAAGAGGG 1349
Qy 1261 GGACACGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGGCCCACTTGGCTCTCTCC 1320
Db 1350 GGACACGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGGCCCACTTGGCTCTCTCC 1409
Qy 1321 TGCTTGGCTGACTGCGGTTCTTGGAACATGTGCAATTTCACTGGGCGCATGGGATCTCATC 1380
Db 1410 TGCTTGGCTGACTGCGGTTCTTGGAACATGTGCAATTTCACTGGGCGCATGGGATCTCATC 1469
Qy 1381 TCCCTTCATCCCGAGCTGGTCTCATCCCTGCGAGGGCCCTTCTTCTGCTCATGGTCT 1440
Db 1470 TCCCTTCATCCCGAGCTGGTCTCATCCCTGCGAGGGCCCTTCTTCTGCTCATGGTCT 1529

Qy 1441 TCAGGTGGCCCTGATCATATGGAAGTAAGGAGTTAGGCATTAACCTTCTGGGAGTGAACCCCTG 1500
Db 1530 TCAGGTGGCCCTGATCATATGGAAGTAAGGAGTTAGGCATTAACCTTCTGGGAGTGAACCCCTG 1589
Qy 1501 ACTCCATCCCTTATTTGGCCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGTAAT 1560
Db 1590 ACTCCATCCCTTATTTGGCCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGTAAT 1649
Qy 1561 TCAACAGTTAAAGAAAGCTTATCTTAAATGTATTTGTTGGGGGTGGGCGAGGCCCACT 1620
Db 1650 TCAACAGTTAAAGAAAGCTTATCTTAAATGTATTTGTTGGGGGTGGGCGAGGCCCACT 1709
Qy 1621 CTATGTTATGTTAAGAGTTGTTCTGGTCTTGGTGTATGTTCTGTATCTTAAACATGAC 1680
Db 1710 CTATGTTATGTTAAGAGTTGTTCTGGTCTTGGTGTATGTTCTGTATCTTAAACATGAC 1769
Qy 1681 CACAGTTTGTAACTAC 1696
Db 1770 CACAGTTTGTAACTAC 1785

RESULT 3

US-09-989-920-56
; Sequence 56, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chonghua
; FILE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-56

Query Match 93.5%; Score 1602.4; DB 3; Length 1977;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;

Qy 1 ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTTCCAGCTTGGGACCGTGGGAG 60
Db 254 ATGCCCGCCCTGGACACCCCGCCAGCATCTGGGCTTCCAGCTTGGGACCGTGGGAG 313
Qy 61 CGGCCAACAGAGCTATGCTGGAGACATATGATAAAACCACTCAGCCCCCACCAGCCGC 120
Db 314 CGGCCAACAGAGCTATGCTGGAGACATATGATAAAACCACTCAGCCCCCACCAGCCGC 373
Qy 121 CGACCCGTAGACACCCAGGACCTGGCCACCATTGGCCAGGCGCAGAGCATTTACCTTC 180
Db 374 CGACCCGTAGACACCCAGGACCTGGCCACCATTGGCCAGGCGCAGAGCATTTACCTTC 433
Qy 181 ATCTCTGGCTCTGCTGAGCCGGCCCTTGTAGTCCCCCACTGCTGCTGCTGCTGCTGCTGCT 240
Db 434 ATCTCTGGCTCTGCTGAGCCGGCCCTTGTAGTCCCCCACTGCTGCTGCTGCTGCTGCTGCT 493
Qy 241 TGGGTGTGGAGTGTGTCGGGCTGCTTCTGCTTCGG-CCGCTGCCGGATTTGCTTCCA 299
Db 494 TGGGTGTGGAGTGTGTCGGGCTGCTTCTGCTTCGGCCGCTGCTGCTGCTGCTGCTGCTGCT 553
Qy 300 GGGCTGTGGA-CCCTGCTGTGCGGGATGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
Db 554 GGGCTGTGGAGGCTGTGTGCGGGATGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613

QY 358 GAGGGAGCTGCTGAAGCCAACTGG -GCCAAGGAGCACAATGGAGTGCGCCCCCAGCCCTGA 416
DB 614 GAGGGAGCTGCTGAAGCCAACTGGTGCCAAAGAGCACAATGGAGTGCGCCCCCAGCCCTGA 673
QY 417 TCGTGACACCCCCAG -CCGCGGGGATGGCCA--GCGGCTCAAGTCAACCATGGGCAGCA 472
DB 674 TCGTGACACCCCCAGACCGCGGGATGGCCAGCGGGCTGCAAGTCAACCATGGGCAGCA 733
QY 473 GCTTCAGCTACCCCGATGTTAAGCTCAAAAGGATCCCTGTGTATCCCTAACCGAG -GGCC 531
DB 734 GCTTCAGCTACCCCGATGTTAAGCTCAAAAGGATCCCTGTGTATCCCTAACCGAGAGGCC 793
QY 532 ACCTCCCAAGCCCTGATCGGAGCTCTGCTGCAAGGAGCCACTGCGCGATCCCCACCC 591
DB 794 ACCTCCCAAGCCCTGATCGGAGCTCTGCTGCAAGGAGCCACTGCGCGATCCCCACCC 853
QY 592 ATGCGA -CACAGCTGCCCCAGCACCTTTTGCCAGTAGTCTCGTGGCTCCGAGGAGTACTA 650
DB 854 ATGCGAGCACGCTGCCCCAGCACCTTTTGCCAGTAGTCTCGTGGCTCCGAGGAGTACTA 913
QY 651 TTCCTTCCATGATCGGAAGCTGGAAGCTGCGCGAGATGGGAGTGGCTCCATGTGAGCGCG 710
DB 914 TTCCTTCCATGATCGGAAGCTGGAAGCTGCGCGAGATGGGAGTGGCTCCATGTGAGCGCG 973
QY 711 AGAAATTGATGTGCTCATCTTCAAGAGAGCTGACAG -GCTGTTCAAGCTACACCCAGATCG 769
DB 974 AGAAATTGATGTGCTCATCTTCAAGAGAGCTGACAGAGGCTGTTCAAGCTACACCCAGATCG 1033
QY 770 ATGAGTGGCCAAAGTGCACATCAGACATGTGTCTCTGGAGAGACCAAGTAAGATCTCGG 829
DB 1034 ATGAGTGGCCAAAGTGCATCAGACATGTGTCTCTGGAGAGACCAAGTAAGATCTCGG 1093
QY 830 ACCTTATCAGCAGCATCAACGAGGACTACCACTGGATGAGCAGGATGCTGAGGGCGGCC 889
DB 1094 ACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGGCGGCC 1153
QY 890 TGGTACCGCGGATCATCTCCATTTAGTACCGGAAGAGCCGTCTGCCCCACAGACCTCGG 949
DB 1154 TGGTACCGCGGATCATCTCCATTTAGTACCGGAAGAGCCGTCTGCCCCACAGACCTCGG 1213
QY 950 AGGGTCGTTCAACTCGGGCTGTGCCCCCAACCGCTGCTGCCCTGACAGTGCGCCATGAGA 1009
DB 1214 AGGGTCGTTCAACTCGGGCTGTGCCCCCAACCGCTGCTGCCCTGACAGTGCGCCATGAGA 1273
QY 1010 CCATGTTGGGCTCAGTCTTCAGCCAGGATGAGCTGACAGTGAGATCTCCAGGAGACGA 1069
DB 1274 CCATGTTGGGCTCAGGCTTCAGCCAGGATGAGCTGACAGTGAGATCTCCAGGAGACGA 1333
QY 1070 CTGCGAGTGCATCGCCCGGAGCTGAGCGCTTATGGAGCTCCAGGGTACCCAGCAAGCC 1129
DB 1334 CTGCGAGTGCATCGCCCGGAGCTGAGGCTTATGGAGCTCCAGGGTACCCAGCAAGCC 1393
QY 1130 ATGACTCATCTTCCAGGGCACCGACACAGACTCGTCGGGGGACCCCTTGCTCCAGGTGT 1189
DB 1394 ATGACTCATCTTCCAGGGCACCGACACAGACTCGTCGGGGGACCCCTTGCTCCAGGTGT 1453
QY 1190 ACTGCTAAACCTTCAGCCAGCTGCGCACACCCCTTTCGGGAGAGCATGCGCTTACAG 1249
DB 1454 ACTGCTAAACCTTCAGCCAGCTGCGCACACCCCTTTCGGGAGAGCATGCGCTTACAG 1513
QY 1250 AATGAGAGGGGACCAAGNACCCCTGTGGGAGGCTTAGACCTGAAGCATGCCCCACT 1309
DB 1514 AATGAGAGGGGACCAAGNACCCCTGTGGGAGGCTTAGACCTGAAGCATGCCCCACT 1573
QY 1310 CTGGCTCTCTCGCTTGGCTGACTGGGTTCTTGAGCCATGTGCAATTTCACTGGGCGATG 1369
DB 1574 CTGGCTCTCTCGCTTGGCTGACTGGGTTCTTGAGCCATGTGCAATTTCACTGGGCGATG 1633
QY 1370 GGATCTACATCTCTTGCATCCCCAGCTGGTCTGATCCCTGCGAGGGCCCTTCCTTCCT 1429
DB 1634 GGATCTACATCTCTTGCATCCCCAGCTGGTCTGATCCCTGCGAGGGCCCTTCCTTCCT 1693

RESULT 4

US-09-989-920-117
; Sequence 117, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Proteins
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989, 920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-117

Query Match 93.5%; Score 1602.4; DB 3; Length 1977;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 6; Indels 11; Gaps 9;

QY 1 ATGCCCGCGCCCTGGACACCCCGCCAGCATCTGGGCTTCCACGCTTGGGACCGTGGGAG 60
DB 254 ATGCCCGCGCCCTGGACACCCCGCCAGCATCTGGGCTTCCACGCTTGGGACCGTGGGAG 313
QY 61 CGGCCAACAGAGCTATGTCTGAGACATATGATAAACACCTCAGCCCCCACCAGCCGC 120
DB 314 CGGCCAACAGAGCTATGTCTGAGACATATGATAAACACCTCAGCCCCCACCAGCCGC 373
QY 121 CGCACCCGTAGACCAGACCCCGAGNCCCTGGCCACCATGGGCCAGAGAGCATTTACCTTC 180
DB 374 CGCACCCGTAGACCAGACCCCGAGNCCCTGGCCACCATGGGCCAGAGAGCATTTACCTTC 433
QY 181 ATCTCTGGCTCTGCTGAGCGCGCCCTTGTAGTCCCCCAGCTGCTGTGCTCTGGCGACCC 240
DB 434 ATCTCTGGCTCTGCTGAGCGCGCCCTTGTAGTCCCCCAGCTGCTGTGCTCTGGCGACCC 493
QY 241 TGGGTGTGGAGTGTGTCGGGCTGCTTCTGCTTCG -CGCTGCGCGGATGTCCTCA 299
DB 494 TGGGTGTGGAGTGTGTCGGGCTGCTTCTGCTTCGCGCGCTGCTGCTGCTGCTGCTGCTCA 553
QY 300 GCGCTGTGGA -GCTGTGTGCGGGATGAGCCCCCTGCTGTACTACTGAGGACT -CCACT 357
DB 554 GCGCTGTGAGGCTGTGTGTGCGGGATGAGCCCCCTGCTGTACTACTGAGGACTTCCACT 613

Qy	358	GAGGGGACTGCTGTAAGCCAACTGG-GCCAAAGGAGCAAAATGGAGTGCCCCCAGCCCTGGA	416
Db	614	GAGGGGACTGCTGTAAGCCAACTGGTGCCAAGAGGACAAATGGAGTGCCCCCAGCCCTGGA	673
Qy	417	TCGTGCACCCCCCCAG-CGGCGGGGATGGCCCA--GCGGCTCAAGTCAACCATGGGAGCA	472
Db	674	TCGTGCACCCCCCCAGACCGGCGGGATGGCCAGGGCGGCTGCAAGTCAACCATGGGAGCA	733
Qy	473	GCTTCAGCTACCCCGATGTTAAGCTCAAAAGGCATCCCTGTGTATCCCTACCCGAG-GGCC	531
Db	734	GCTTCAGCTACCCCGATGTTAAGCTCAAAAGGCATCCCTGTGTATCCCTACCCGAGAGGCC	793
Qy	532	ACCTCCCGAGCCCTGTATGCGGACTCTCTGTGCAAGAGGCACATGGGCGGATGCCCCACCC	591
Db	794	ACCTCCCGAGCCCTGTATGCGGACTCTCTGTGCAAGAGGCACATGGGCGGATGCCCCACCC	853
Qy	592	ATGCGA-CACAGCCTGCCACGACCTTTTCCAGTAGTCTCTGTGGCTCCGAGGAGTACTA	650
Db	854	ATGCGAGACAGCCTGCCACGACCTTTTCCAGTAGTCTCTGTGGCTCCGAGGAGTACTA	913
Qy	651	TTCTTTTCCATGAGTCGGACCTTGGACCTTCCCGGAGATGGGCAAGTGGCTCCAATGTGAGCCG	710
Db	914	TTCTTTTCCATGAGTCGGACCTTGGACCTTCCCGGAGATGGGCAAGTGGCTCCAATGTGAGCCG	973
Qy	711	AGAAATGATGTGCTCATCTTTCAAGAGCTGACAGA-GCTGTTTCAGCGGTACACAGATCG	769
Db	974	AGAAATGATGTGCTCATCTTTCAAGAGCTGACAGAGGCTGTTTCAGCGGTACACAGATCG	1033
Qy	770	ATGAGCTGGCCAAAGTGCATCAGACACTGTGTTCTTGGAGAGACAGATGAGTACTCGG	829
Db	1034	ATGAGCTGGCCAAAGTGCATCAGACACTGTGTTCTTGGAGAGACAGATGAGTACTCGG	1093
Qy	830	ACCTTTATCAGCAGCATACGCGAGCTACCACTGGATGAGCAGGATGCTTGAGGGCCGCC	889
Db	1094	ACCTTTATCAGCAGCATACGCGAGCTACCACTGGATGAGCAGGATGCTTGAGGGCCGCC	1153
Qy	890	TGGTACCGGGCATCATTTGCGATTAGTACCCGAAAGACCGGTGCTCGCCCAAGACCTCTCGG	949
Db	1154	TGGTACCGGGCATCATTTGCGATTAGTACCCGAAAGACCGGTGCTCGCCCAAGACCTCTCGG	1213
Qy	950	AGGTCGTTTCAACTCGGGGCTGCTGCCCAACCGCTGTGCCCCCTGACAGTGGCCATGAGA	1009
Db	1214	AGGTCGTTTCAACTCGGGGCTGCTGCCCAACCGCTGTGCCCCCTGACAGTGGCCATGAGA	1273
Qy	1010	CCATGTTGGGCTCAGGTCCTCAGCCAGGATGAGCTGCAGTGCAGATCTCCAGGAGACGA	1069
Db	1274	CCATGTTGGGCTCAGGTCCTCAGCCAGGATGAGCTGCAGTGCAGATCTCCAGGAGACGA	1333
Qy	1070	CTGCAGATGCCATCCGCCGGAAGCTGAGGCTTTATGGAGTCTCAGGTTACCCAGCAAGCC	1129
Db	1334	CTGCAGATGCCATCCGCCGGAAGCTGAGGCTTTATGGAGTCTCAGGTTACCCAGCAAGCC	1393
Qy	1130	ATGACTCATCTTCCAGGGCACCGACACAGACTCGTTCGGGGGACCCCTTGTCTCAGGTGT	1189
Db	1394	ATGACTCATCTTCCAGGGCACCGACACAGACTCGTTCGGGGGACCCCTTGTCTCAGGTGT	1453
Qy	1190	ACTGCTAAACCCCTGCCAGGCCAGCTGCACACCCCTTTTCTGGGAGAGCATGGCCTACAG	1249
Db	1454	ACTGCTAAACCCCTGCCAGGCCAGCTGCACACCCCTTTTCTGGGAGAGCATGGCCTACAG	1513
Qy	1250	AATGAAGAGGGGGACGAGGAACCCCTGTGGAGAGGCTTAGACTGCAAGCAGATGCCCACT	1309
Db	1514	AATGAAGAGGGGGACGAGGAACCCCTGTGGAGAGGCTTAGACTGCAAGCAGATGCCCACT	1573
Qy	1310	CTGGCTCTCTGTGCTTGTGCTGACTGGGTTCTTGGAAGATGTGCAATTTCACTGGGCCATG	1369
Db	1574	CTGGCTCTCTGTGCTTGTGCTGACTGGGTTCTTGGAAGATGTGCAATTTCACTGGGCCATG	1633
Qy	1370	GGATCTACATCTCTTCGATCCCGAGCTGGTCTGATCCCTGCCAGGGGCCCTTCTTCTCT	1429
Db	1634	GGATCTACATCTCTTCGATCCCGAGCTGGTCTGATCCCTGCCAGGGGCCCTTCTTCTCT	1693
Qy	1430	GCTCATGGTCTTTCAGGTGGGCTGATCATGAAAGATTAAGGAGTTAGGCAATTAACCTTCTGGG	1489

Db	1694	GCTCATGGTCTTCCAGTGGGCGTGCATCATGAAAGTAAGGAGTTAGGCATTACCTTCTGGG	17533
QY	1490	AGTGAACCCCTGACTCCATCCCCCTATTGGCCACCCCTAACCAATCATGCAGAACTTCTCCCTC	15498
Db	1754	AGTGAACCCCTGACTCCATCCCCCTATTGGCCACCCCTAACCAATCATGCAGAACTTCTCCCTC	18133
QY	1550	CCTGGGGTAAATTCAACAGTTAAAAAGAGCTTATCTTAAATGTATTGTATTGGGGGGTGGG	16099
Db	1814	CCTGGGGTAAATTCAACAGTTAAAAAGAGCTTATCTTAAATGTATTGTATTGGGGGGTGGG	18733
QY	1610	CAGGGCCACTCTATGTATTGTAAAGAGTTGGTCTGGTCTTGGCTGTATGTCTGTAT	16598
Db	1874	CAGGGCCACTCTATGTATTGTAAAGAGTTGGTCTGGTCTTGGCTGTATGTCTGTAT	19333
QY	1670	CTTAAACATGACCACAGTTTGTAACTACCTCGGCCGCGACCAACGC	1713
Db	1934	CTTAAACATGACCACAGTTTGTAACTACCTCGGCCGCGACCAACGC	1977
RESULT 5			
US-10-074-475-124			
; Sequence 124, Application US/10074475			
; Publication No. US2003009289A1			
; GENERAL INFORMATION:			
; APPLICANT: Salceda, Susana			
; APPLICANT: Macina, Roberto			
; APPLICANT: Hu, Ping			
; APPLICANT: Recipon, Herve			
; APPLICANT: Karra, Kalpana			
; APPLICANT: Cafferkey, Robert			
; APPLICANT: Sun, Yongming			
; APPLICANT: Liu, Chenghua			
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific			
; FILE REFERENCE: DEX-0313			
; CURRENT APPLICATION NUMBER: US/10/074,475			
; CURRENT FILING DATE: 2002-02-13			
; PRIOR APPLICATION NUMBER: 60/268,292			
; PRIOR FILING DATE: 2001-02-13			
; NUMBER OF SEQ ID NOS: 295			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 124			
; LENGTH: 654			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-10-074-475-124			

Query Match	35.5%;	Score 607.6;	DB 5;	Length 654;
Best Local Similarity	96.6%;	Pred. No. 5.1e-178;		
Matches 632;	Conservative 0;	Mismatches 19;	Indels 3;	Gaps 1;
Qy	89	ATGATAAACACCTCAGCCCCCACCACCGCCGCGCACCCGTAGACCAGACCCCAAGGACC	148	
Db	1	ATGATAAACACCTCAGCCCCCACCACCGCCGCGCACCCGTAGACCAGACCCCAAGGACC	60	
Qy	149	CTGGCCACCATGGCCAGAGAGCATTAACCTTTCATCTCTGGCTCTGCTGAGCGCGGCCCTTG	208	
Db	61	CTGGCCACCATGGCCAGAGAGCATTAACCTTTCATCTCTGGCTCTGCTGAGCGCGGCCCTTG	120	
Qy	209	AGTCCCCACCTGCTGCTCTCTGGCGACCCCTGGGTGTGGGAGTGTGTGGCGGCTGCCT	268	
Db	121	AGTCCCCACCTGCTGCTCTCTGGCGACCCCTGGGTGTGGGAGTGTGTGGCGGCTGCCT	180	
Qy	269	TCGTCTTCGCGCGCTGCCGGGATTCCTTCAGCGCTGTGAGCCTGTGTGGGGGATGCA	328	
Db	181	TCTGCTTTCGCGCGCTGCCGGGATTCCTTCAGCGCTGTGAGGCGCTGTGCGGGGATGCA	240	
Qy	329	GCCTTCGCTGTCTACTGAGGACTTCCACTCAGGGGACTGTGTAAGCCAACTGGGCCCAAGG	388	
Db	241	GCCTTCGCTGTCTACTGAGGACTTCCCTGAGGGGACTGTGTAAGCCAACTGTGTCCAAGG	300	
Qy	389	AGCACAATGAGGTGCCCCCGACGCCCTGATGCTGCACCCCCCGACCGCGGGATGGCCA--	446	

301	Db		AGCACAAATGGAGTGGCCCCCAGCCCTGATCGTCAGCCCCCGCGCGGGATGGCCAGG	360
447	Qy	-GGGGCTCAAGTCAACCATGGGCAGCAGCTTCAGCTACCCCGATGTTTAAGCTCAAAAGGCA	505	
361	Db	CGGGCTGCAAGTCAACCATGGGCAGCAGCTTCAGCTACCCCGATGTTTAAGCTCAAAAGGCA	420	
506	Qy	TCCCTGTGTATCCCTACCCGAGGGGCACCTCCCGAGCCCTGTATCGGAGACTCTCTGTGCA	565	
421	Db	TCCCTGTGTATCCCTACCCGAGAGGCCACCTCCCGAGCCCTGTATCGGAGACTCTCTGTGCA	480	
566	Qy	AGGAGCCACTGGCGGATCCCCCACCACCATGGGCAGCAGGCTGCCAGCAGCACCTTTGCCAGTA	625	
481	Db	AGGAGCCACTGGCGCGATCCCCCACCACCCAGCAGCAGCCTGCCAGCAGCACCTTTGCCAGTA	540	
626	Qy	GTCTCTGGTCTCCGAGAGTAGTACTATCTTTCCATGATCGGACCTGGACCTCCCGGAGA	685	
541	Db	GTCTCTGGTCTCCGAGAGTAGTACTATCTTTCCATGATCGGACCTGGACCTCCCGGAGA	600	
686	Qy	TGGCAGTGGCTCCATGTGAGCCGAGAAATTGATGTGCTCATCTTCAAGAAGC	739	
601	Db	TGGCAGTGGCTCCATGTGAGCCGAGAAATTGATGTGCTCATCTTCAAGAAGC	654	

RESULT 6

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US-10-779-543-5731
; Sequence 5731, Application US/10779543
; Publication No. US20050227917A1
GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5731
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 15, 16, 17, 18, 20,
; LOCATION: 22, 23, 24, 25, 28, 29, 30, 36, 41, 85, 89, 97, 106, 108,
; LOCATION: 115, 134, 139, 177, 185, 207, 232, 275, 283, 303, 320, 32
; LOCATION: 356, 414, 451, 469, 551, 566, 582, 588, 591, 605, 631, 65
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 663, 678, 684, 687, 689, 702, 706, 710, 711, 713, 722
; OTHER INFORMATION: n = A,T,C or G

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US-09-989-920-55			
Query Match 22.5%; Score 385; DB 3; Length 385;			
Best Local Similarity 100.0%; Pred. No. 8e-109;			
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1190	ACTGCTAACCCCTGCCAGGCCAGCTGCCACACCCCTTCTCTGGGAGAGCATGGCCTACAG	1249
Db	1	ACTGCTAACCCCTGCCAGGCCAGCTGCCACACCCCTTCTCTGGGAGAGCATGGCCTACAG	60
Qy	1250	AATGAAGAGGGGACACAGGAACCCCTCTGGAGAGGCTTAGACCTGAAGCAGTGGCCCACT	1309
Db	61	AATGAAGAGGGGACACAGGAACCCCTCTGGAGAGGCTTAGACCTGAAGCAGTGGCCCACT	120
Qy	1310	CTGGCTCCTCTCTGGCTTGGCTGACTCTGGATCTCTGGACCATGTGCAATTCATCTGGGCCATG	1369
Db	121	CTGGCTCCTCTCTGGCTTGGCTGACTCTGGATCTCTGGACCATGTGCAATTCATCTGGGCCATG	180
Qy	1370	GGATCTACATCTCTTTCATCTCCCGACCTGCTGATCCCTGCCAGGGCCCTTCTTCCT	1429
Db	181	GGATCTACATCTCTTTCATCTCCCGACCTGCTGATCCCTGCCAGGGCCCTTCTTCCT	240
Qy	1430	GCTCATCGTCTTCAGGTGGCTGATCATGAAAGTAAGGAGTTAGGCATTTACCTTCTGGG	1489
Db	241	GCTCATCGTCTTCAGGTGGCTGATCATGAAAGTAAGGAGTTAGGCATTTACCTTCTGGG	300
Qy	1490	AGTGAACCCCTGACTCCATCCCTTATTTGCCACCCCTAACCAATCATGCAAACTTCTCCCTC	1549
Db	301	AGTGAACCCCTGACTCCATCCCTTATTTGCCACCCCTAACCAATCATGCAAACTTCTCCCTC	360
Qy	1550	CTGGGGTAAATCAACAGTTAAAG	1574
Db	361	CTGGGGTAAATCAACAGTTAAAG	385
RESULT 8			
US-09-989-890-104			
; Sequence 104, Application US/09989890			
; Publication No. US20040166105A1			
; GENERAL INFORMATION:			
; APPLICANT: Salceda, Susana			
; APPLICANT: Macina, Roberto			
; APPLICANT: Recipon, Herve			
; APPLICANT: Pluta, Jason			
; APPLICANT: Sun, Yongming			
; APPLICANT: Liu, Chenghua			
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and			
; FILE REFERENCE: DEX-0287			
; CURRENT APPLICATION NUMBER: US/09/989,890			
; CURRENT FILING DATE: 2001-11-21			
; PRIOR APPLICATION NUMBER: 60/252,509			
; PRIOR FILING DATE: 2000-11-22			
; NUMBER OF SEQ ID NOS: 280			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 104			
; LENGTH: 386			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-989-890-104			
Query Match 22.2%; Score 380.2; DB 3; Length 386;			
Best Local Similarity 99.2%; Pred. No. 2.5e-107;			
Matches 382; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	1196	AACCCCTGCCAGGCCAGCTGCCACACCCCTTCTCTGGGAGAGCATGGCCTACAGAATGAA	1255
Db	2	ACCCCTGGCCAGGCCAGCTGCCACACCCCTTCTCTGGGAGAGCATGGCCTACAGAATGAA	61
Qy	1256	GAGGGGACACAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGGCCCACTCTGGCT	1315
Db	62	GAGGGGACACAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGGCCCACTCTGGCT	121
Qy	1316	CTCTCTCCCTTGGCTGACTGGGTCTCTGGACCATGTGCATTTCACTGGGCCATGGGATCT	1375

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Db 302 CCTGACTCATCCCTATTGTCACCCCTAAACCAATCATGCAAACTTCTCCCTCCCTGGG 361
QY 1556 GTAATTCACAGTTAAAGAAGCTT 1580
Db 362 GTAATTCACAGTTAAAGAAGCTT 386

RESULT 10
US-10-779-543-10096
; Sequence 10096, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR FILING DATE: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1997-12-23
; PRIOR FILING DATE: 1997-12-23
; PRIOR FILING DATE: 1997-12-23
; PRIOR FILING DATE: 1998-04-03
; PRIOR FILING DATE: 1998-04-03
; PRIOR FILING DATE: 1998-04-03
; PRIOR FILING DATE: 1998-10-21
; PRIOR FILING DATE: 1998-10-21
; PRIOR FILING DATE: 1998-10-21
; PRIOR FILING DATE: 1998-01-28
; PRIOR FILING DATE: 1999-01-28
; PRIOR FILING DATE: 1998-01-28
; PRIOR FILING DATE: 1998-01-28
; PRIOR FILING DATE: 1998-02-24
; PRIOR FILING DATE: 1998-02-24
; PRIOR FILING DATE: 1998-03-31
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10096
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 355
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-10096

Query Match 20.6%; Score 352.6; DB 9; Length 393;
Best Local Similarity 98.4%; Pred. No. 9.8e-99;
Matches 366; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 805 CTGGAGAACACAGTAAGTCTCGGACCTTATCAGCAGCATCAGCAGCACTACCACTG 864
Db 21 CTGGAGAACCAGTAAGATCTCGGACCTTATCAGCAGCATCAGCAGCACTACCACTG 80

QY 865 GATGACAGGATGCTCAGGCGCCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAG 924
Db 81 GATGACAGGATGCTGAGGCGCCCTGGTACGCGGCATCATTCGCATTAGTACCCGAAAG 140

QY 925 AGCCGTGCTCGGCCACAGACCTCGGAGGGTGGTTCAACTCGGCTGCTGCCCAACCGCT 984
Db 141 AGCCGTGCTCGGCCACAGACCTCGGAGGGTGGTTCAACTCGGCTGCTGCCCAACCGCT 200

QY 985 GCTGCCCCCTGACAGTGGCCATGACATGCTGGGCTCAGGTCTCAGCCAGGATGAGCTG 1044
Db 201 GCTGCCCCCTGACAGTGGCCATGACATGCTGGGCTCAGGTCTCAGCCAGGATGAGCTG 260

QY 1045 ACAGTGCAGATCTCCCAAGGAGACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCCCTTAT 1104
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Db 261 ACAGTGCAGATCTCCCAAGGAGACGACTGCAGATGCCATGCCGGAAGCTGAGCCCTTAT 320
QY 1105 GGAGCTCCAGGTACCCAGCAAGCCATGACTCATCTTCCA-GGGCACGACACAGACTC 1163
Db 321 GGAGCTCCAGGTACCCAGCAAGCCATGACTCATCTTTCAGGGGCACGACAGACTC 380
QY 1164 GTCGGGGGCACC 1175
Db 381 GTCGGGGGCACCC 392

RESULT 11
US-10-779-543-12051
; Sequence 12051, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR FILING DATE: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1997-12-23
; PRIOR FILING DATE: 1997-12-23
; PRIOR FILING DATE: 1998-04-03
; PRIOR FILING DATE: 1998-04-03
; PRIOR FILING DATE: 1998-10-21
; PRIOR FILING DATE: 1998-10-21
; PRIOR FILING DATE: 1998-10-21
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; PRIOR FILING DATE: 1999-01-28
; PRIOR FILING DATE: 1998-01-28
; PRIOR FILING DATE: 1998-01-28
; PRIOR FILING DATE: 1998-02-24
; PRIOR FILING DATE: 1998-02-24
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12051
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-12051

Query Match 20.3%; Score 347; DB 9; Length 427;
Best Local Similarity 99.7%; Pred. No. 5.6e-97;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCCGCCCTGGACACCCCGCCCGCAGCATCTGGGCTTCCACGCTTGGGACCGTGGGAG 60
Db 80 ATGCCCGCCCTGGACACCCCGCCCGCAGCATCTGGGCTTCCACGCTTGGGACCGTGGGAG 139

QY 61 CGGCCAACAGAGCTATGCTTGAGACATATGATAAACACCTCAGCCCCCACCAGCCGC 120
Db 140 CGGCCAACAGAGCTATGCTTGAGACATATGATAAACACCTCAGCCCCCACCAGCCGC 199

QY 121 CGCACCGGTAGACACCCCGCCCGCAGGACCTGGCCACCATGGGCGCAGAGCATTTACCTTC 180
Db 200 CGCACCGGTAGACACCCCGCCCGCAGGACCTGGCCACCATGGGCGCAGAGCATTTACCTTC 259

QY 181 ATCTCTGGCTCTGCTGAGCGCGGCCCTTGTAGTCCCCCACCCTGTGCTGTGGCGACCC 240
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QY 980 CGCTGCTGCCCTGACAGTGGCCATGAGACCATGCTGGGCTCAGGTCTCAGCCAGGATG 1039
Db 241 CGCTGCTGCCCTGACAGTGGCCATGAGACCATGCTGGGCTCAGGTCTCAGCCAGGATG 300

RESULT 14
US-10-779-543-34
; Sequence 34, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALY EXPRESSED
; FILE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; TITLE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-779-543-34

Query Match 17.4%; Score 298.4; DB 9; Length 300;
Best Local Similarity 99.7%; Pred. No. 6.6e-82;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGCAGAGCTGTTACGGGTACACCAGATCGATGAGTGGCCAGTGCATCAGACACTG 799
Db 1 TGCAGAGCTGTTACGGGTACACCAGATCGATGAGTGGCCAGTGCATCAGACACTG 60

QY 800 TGTTCCTGGAGAGACAGTAAGATCTCGGACCTTATCAGCAGCATCAGCCAGGACTACC 859
Db 61 TGTTCCTGGAGAGACAGTAAGATCTCGGACCTTATCAGCAGCATCAGCCAGGACTACC 120

QY 860 ACTGGATGAGCAGGATGCTGAGGGCCGCTGTGTA CGCGGATCATTCGATTTAGTACC 919
Db 121 ACCTGGATGAGCAGGATGCTGAGGGCCGCTGTGTA CGCGGATCATTCGATTTAGTACC 180

QY 920 GAAAGAGCGTGTCTCGCCACAGACATCGGAGGCTGTTCACTCGGGCTGCGCCCAA 979
Db 181 GAAAGAGCGTGTCTCGCCACAGACATCGGAGGCTGTTCACTCGGGCTGCGCCCAA 240

QY 980 CGCTGCTGCCCTGACAGTGGCCATGAGACCATGCTGGGCTCAGGTCTCAGCCAGGATG 1039
Db 241 CGCTGCTGCCCTGACAGTGGCCATGAGACCATGCTGGGCTCAGGTCTCAGCCAGGATG 300
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RESULT 15
US-09-989-920-116/c

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; Sequence 116, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Proteins
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 116
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-116

Query Match 7.0%; Score 120; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.6e-26;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 AAGCTTATCTTAAATCTATTGTTGGGGGTGGGCAGGGCCCACTCTATGTTATGTTAA 1634
Db 120 AAGCTTATCTTAAATGTTATTGTTGGGGGTGGGCAGGGCCCACTCTATGTTATGTTAA 61

QY 1635 GGAGTTGGTTCCTGGTTCCTGGCTGATGTTCTGTATCTTAACATGACACAGTTTGAAGT 1694
Db 60 GGAGTTGGTTCCTGGTTCCTGGCTGATGTTCTGTATCTTAACATGACACAGTTTGAAGT 1

Search completed: March 11, 2006, 22:42:56
Job time : 1289 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 20:00:54 ; Search time 591 Seconds
(without alignments)
6687.647 Million cell updates/sec

Title: US-09-989-890-105

Perfect score: 1713

Sequence: 1 atgccccgcctggacaccc.....tactcggccgcgacacgc 1713

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_New.*
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1592.8	98.8	1785	9	US-11-072-512-799 Sequence 799, App
2	40.6	2.4	1738	12	US-10-501-035-144 Sequence 144, App
3	40.4	2.4	3320	12	US-11-124-368A-154 Sequence 154, App
4	40.4	2.4	3338	12	US-11-124-368A-156 Sequence 156, App
5	40.4	2.4	3422	12	US-11-124-368A-155 Sequence 155, App
6	38.6	2.3	587	6	US-09-925-065A-893863 Sequence 893863, App
7	38.6	2.3	590	6	US-09-925-065A-894029 Sequence 894029, App
8	38.6	2.3	5706	12	US-11-052-554A-519 Sequence 519, App
9	37.8	2.2	15234	12	US-11-136-527-306 Sequence 306, App
10	37.6	2.2	1431	9	US-11-096-568A-22110 Sequence 22110, App
11	37.6	2.2	38239	7	US-10-330-773-603 Sequence 603, App
12	37.4	2.2	37507	8	US-10-522-037-2 Sequence 2, Appl
13	37.2	2.2	1067	6	US-09-925-065A-551694 Sequence 551694, App
14	37.2	2.2	162173	12	US-11-121-086-72 Sequence 72, Appl
15	37	2.2	6034	7	US-10-501-035-200 Sequence 200, App
16	36.6	2.1	566	6	US-09-925-065A-732134 Sequence 732134, App
17	36.6	2.1	656	6	US-09-925-065A-56292 Sequence 56292, App
18	36.4	2.1	2859	8	US-10-995-561-314 Sequence 314, App
19	36.4	2.1	2941	8	US-10-995-561-315 Sequence 315, App
20	36.4	2.1	3240	12	US-11-052-554A-529 Sequence 529, App

C 21	36.4	2.1	21442	8	US-10-995-561-13469 Sequence 13469, A
C 22	36.4	2.1	35770	12	US-10-995-561-13296 Sequence 13296, A
C 23	36.4	2.1	77246	12	US-11-124-368A-2907 Sequence 2907, App
C 24	36.2	2.1	566	6	US-09-925-065A-732133 Sequence 732133, App
C 25	36	2.1	2745	7	US-10-921-793-73 Sequence 73, Appl
C 26	36	2.1	2745	7	US-10-931-198-73 Sequence 73, Appl
C 27	36	2.1	2745	8	US-10-517-544-76 Sequence 76, Appl
C 28	36	2.1	13884	8	US-10-995-561-13376 Sequence 13376, A
C 29	35.8	2.1	2323	8	US-10-750-185-31877 Sequence 31877, A
C 30	35.8	2.1	2323	8	US-10-750-623-31877 Sequence 31877, A
C 31	35.8	2.1	2552	8	US-10-750-185-55078 Sequence 55078, A
C 32	35.8	2.1	2552	8	US-10-750-623-55078 Sequence 55078, A
C 33	35.8	2.1	3309	9	US-11-072-512-977 Sequence 977, App
C 34	35.8	2.1	6076	12	US-11-136-527-2597 Sequence 2597, App
C 35	35.6	2.1	536	6	US-09-925-065A-535967 Sequence 535967, App
C 36	35.6	2.1	614	6	US-09-925-065A-681562 Sequence 681562, App
C 37	35.6	2.1	138627	7	US-10-330-773-159 Sequence 159, App
C 38	35.4	2.1	1404	8	US-10-750-185-56117 Sequence 56117, A
C 39	35.4	2.1	1404	8	US-10-750-623-56117 Sequence 56117, A
C 40	35.4	2.1	355211	7	US-10-330-773-242 Sequence 242, App
C 41	35.2	2.1	632	6	US-09-925-065A-841922 Sequence 841922, App
C 42	35.2	2.1	1225	8	US-10-750-185-24937 Sequence 24937, A
C 43	35.2	2.1	1225	8	US-10-750-623-24937 Sequence 24937, A
C 44	35.2	2.1	1429	7	US-10-973-115B-485 Sequence 485, App
C 45	35.2	2.1	1429	8	US-10-131-826A-485 Sequence 485, App

ALIGNMENTS

RESULT 1

US-11-072-512-799
; Sequence 799, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAL, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 799
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-799

Query Match 98.8%; Score 1692.8; DB 9; Length 1785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCCCCGCCCTGGACACACCCCGCCAGCATCTGGCCCTCCACGCTTGGAGCCGTGGGAG 60
DB |||||
90 ATGCCCGGCCCTGGACACACCCCGCCAGCATCTGGCCCTCCACGCTTGGAGCCGTGGGAG 149
QY CGGCCAACAGAGCTATGCTGGAGACATATGATAAACAACCTCAGCCCCCACAAGCCGC 120
DB |||||
150 CGGCCAACAGAGCTATGCTGGAGACATATGATAAACAACCTCAGCCCCCACAAGCCGC 209
QY 121 CGCACCCGTAGACACAGACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCATTAACCTTC 180
DB |||||
210 CGCACCCGTAGACACAGACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCATTAACCTTC 269
QY 181 ATCTCTGGCTCTGCTGAGCGCGCCCTTGAATCCCCCACTGCTGCTCTGGCGACCC 240
DB |||||
270 ATCTCTGGCTCTGCTGAGCGCGCCCTTGAATCCCCCACTGCTGCTCTGGCGACCC 329
QY 241 TGGGTGTGGAGTGTGCGCGGCTGCTTCTGCTTCCGCGCTGCGCGGATTTGCCCTCCAG 300
DB |||||
330 TGGGTGTGGAGTGTGCGCGGCTGCTTCTGCTTCCGCGCTGCGCGGATTTGCCCTCCAG 389
QY 301 CGCTGTGGAGCTGTGCGGGATGACGCCCTGCTGCTACTGAGACTCCACTGAG 360
DB |||||
390 CGCTGTGGAGCTGTGCGGGATGACGCCCTGCTGCTACTGAGACTCCACTGAG 449
QY 361 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCAATGGAGTGCCTCCAGCCCTGATCGT 420
DB |||||
450 GGGACTGCTGAAGCCAACTGGGCCAAGGAGCAATGGAGTGCCTCCAGCCCTGATCGT 509
QY 421 GCACCCCCCAGCGCGGGATGCGCAGCGGCTCAAGTCAACCATGGCGAGCAGCTTCAGC 480
DB |||||
510 GCACCCCCCAGCGCGGGATGCGCAGCAGCTCAAGTCAACCATGGCGAGCAGCTTCAGC 569
QY 481 TACCCCGATGTTAAGCTCAAGGCATCCCTGTGTATCCCTACCCGAGGCGCACTCCCA 540
DB |||||
570 TACCCCGATGTTAAGCTCAAGGCATCCCTGTGTATCCCTACCCGAGGCGCACTCCCA 629
QY 541 GCGCTGTAGCGGACTCTGCTCAAGGAGCCACTGGCGGATGCCCGATCCCGACACAC 600
DB |||||
630 GCGCTGTAGCGGACTCTGCTCAAGGAGCCACTGGCGGATGCCCGATCCCGACACAC 689
QY 601 AGCTGCCCAGCACCTTTGCCAGTAGTCTCTGCTGCTCCGAGGAGTACTTCTTTCCAT 660
DB |||||
690 AGCTGCCCAGCACCTTTGCCAGTAGTCTCTGCTGCTCCGAGGAGTACTTCTTTCCAT 749
QY 661 GAGTCCGACCTGGACCTGCGGAGATGGGCGAGTGGCTCCATGTCGAGCCGAGAAATGAT 720
DB |||||
750 GAGTCCGACCTGGACCTGCGGAGATGGGCGAGTGGCTCCATGTCGAGCCGAGAAATGAT 809
QY 721 GTGCTCATCTTCAAGAGCTGCAGAGCTGTTTCAAGGTTACACAGATCGATGAGCTGGCC 780
DB |||||
810 GTGCTCATCTTCAAGAGCTGCAGAGCTGTTTCAAGGTTACACAGATCGATGAGCTGGCC 869
QY 781 AAGTGACATCAGACACTGTGTTCTTGGAGAAGACCAAGTAAAGATCTCGGACCTTATCAGC 840
DB |||||
870 AAGTGACATCAGACACTGTGTTCTTGGAGAAGACCAAGTAAAGATCTCGGACCTTATCAGC 929
QY 841 AGCATCAGCAGGACTACACCTGGATGAGCAGGATGCTGAGGGCCGCTGTGATCGCGGC 900
DB |||||
930 AGCATCAGCAGGACTACACCTGGATGAGCAGGATGCTGAGGGCCGCTGTGATCGCGGC 989
QY 901 ATCATTTCCGATATGATCCCGAAGAGCCGTGCTCGCCCAACAGACCTCGGAGGCTCGTTCA 960
DB |||||
990 ATCATTTCCGATATGATACCGAAGAGCCGTGCTCGCCCAACAGACCTCGGAGGCTCGTTCA 1049
QY 961 ACTCGGGCTGCTGCCCAACCGCTGCTGCCCTTGAACAGTGGCCATGAGACCATGTTGGGC 1020
DB |||||
1050 ACTCGGGCTGCTGCCCAACCGCTGCTGCCCTTGAACAGTGGCCATGAGACCATGTTGGGC 1109
QY 1021 TCAGTCTCAGCCAGGATGAGTGAACAGTGCAGATCTCCAGGAGACGATGAGATGCC 1080
DB |||||
1110 TCAGTCTCAGCCAGGATGAGTGAACAGTGCAGATCTCCAGGAGACGATGAGATGCC 1169
QY 1081 ATCGCCCGGAAGCTGAGGCTTATGAGCTCCAGGGTACCAGCAAGCCATGATCATCC 1140

DB 1170 ATCGCCCGAAGCTGAGGCTTATGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 1229
QY 1141 TTCCAGGGCACCGACACAGACTCGTCGGGGGACCCCTTCTCCAGGTGTACTGCTAAACC 1200
DB 1230 TTCCAGGGCACCGACACAGACTCGTCGGGGGACCCCTTCTCCAGGTGTACTGCTAGCC 1289
QY 1201 CTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAAGCATGGCTACAGAATGAAGAGG 1260
DB 1290 CTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAAGCATGGCTACAGAATGAAGAGG 1349
QY 1261 GGACCAAGAACCCCTGTGGAGAGGCTTAGAAGCTGAAAGCAGTGCCACCTCTGGCTCTCC 1320
DB 1350 GGACCAAGAACCCCTGTGGAGAGGCTTAGAAGCTGAAAGCAGTGCCACCTCTGGCTCTCC 1409
QY 1321 TGCCTTGGCTGACTGGGTTCTTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 1380
DB 1410 TGCCTTGGCTGACTGGGTTCTTGGACCATGTGCATTTCACTGGGCCATGGGATCTACATC 1469
QY 1381 TCTTGTGATCCCGAGCTGTGATCCCTGCGAGGGCCCTTCTTCTTCTGCTCATGCTCT 1440
DB 1470 TCTTGTGATCCCGAGCTGTGATCCCTGCGAGGGCCCTTCTTCTTCTGCTCATGCTCT 1529
QY 1441 TCAGGTGGCTGATCATGGAAGTAGGAAGTTAGGAGTTAGGCATTTACCTTCTGGAGTGAAACCTTG 1500
DB 1530 TCAGGTGGCTGATCATGGAAGTAGGAAGTTAGGAGTTAGGCATTTACCTTCTGGAGTGAAACCTTG 1589
QY 1501 ACTCATCCCCCTATTTGCCACCTAACCATCATGCAAACTTCTCCCTCCCTGGGGTAAT 1560
DB 1590 ACTCATCCCCCTATTTGCCACCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAT 1649
QY 1561 TCAACAGTTAAAGAGCTTATCTTAAATGATTTGTTGGGGGTGGGAGGCCCACT 1620
DB 1650 TCAACAGTTAAAGAGCTTATCTTAAATGATTTGTTGGGGGTGGGAGGCCCACT 1709
QY 1621 CTATGTTATGTTAAGGAGTTGTTCTTGGTTCTTGGCTGATGTTCTGTATCTTAAACATGAC 1680
DB 1710 CTATGTTATGTTAAGGAGTTGTTCTTGGTTCTTGGCTGATGTTCTGTATCTTAAACATGAC 1769
QY 1681 CACAGTTTGTAAAGTAC 1696
DB 1770 CACAGTTTGTAAAGTAC 1785

RESULT 2

US-10-501-035-144
; Sequence 144, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASES
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 144
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-501-035-144

Query Match 2.4%; Score 40.6; DB 7; Length 1738;
Best Local Similarity 48.1%; Pred. No. 0.76;
Matches 214; Conservative 0; Mismatches 219; Indels 12; Gaps 3;
QY 2 TGCCCCCGCCCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGAGCCGTGGGAGC 61
DB 188 TGACAGCTGCTGGCCCCCCCCCTTCCCGTGTGGGCTGGACTCCCGGG---GGGTGGC 244

62	Qy	GGCCACAGAGCTATGTCTGGAGACATATGATAAACACACTTCAGCCCCCAACCAAGCGCGC	121
245	Db	 GGCCTCATGAATCCCTTCCCGCACCTCAGGGTCACGCCAGAACCCCTTCAGAGTCGGG	304
122	Qy	GCACCGTAGACACAGACCCCAAGGACCTGTGCCACCATGGGCCAGAGAGCATTAACCTTCA	181
305	Db	 GCTGAGCTCCAGTCCGGCTTCTTTGGCTCCAGGGCTGGCCCCAGATCTCATTTCCAGGCG	364
182	Qy	TTCTTGCGCTCTGCTGAGCGCGGCCCTTGAGTCCCCCACTGCTGCCTGCTCTCGCGCACCTT	241
365	Db	 GCGCGCGCGCCCCCGCCACGCCCCAGGCCCCGCGCGCGAGGCCCTCCAGGTGGACTTG	424
242	Qy	GGGTGTGGAGTGTGTGCGGGCTGCTTCTGCTTCGCGCGCTGCGGGATGTGCTTCAGC	301
425	Db	 CTCCCGGTGCTCCGCGCGGCCCCAGGAGTCCGCGCGGTGCTGCGGCGCTGCGCGCGCT	484
302	Qy	GCTGTGGAGCCGTGTGTGGGGGATGCAGCCCTTCGCTG---TCTACTGAGGAGTC---	353
485	Db	 GCTGCCCGCGTGCCTGTGCGCGCCCCCGGCCCTCTGCGCGGCTCTACCGTGTGACACAGCG	544
354	Qy	-CACTTGAGGGAGTGTGTAAGCCAACTGGGCCAAGGAGCAAAATGGAGTGTCCCCCAGCGC	412
545	Db	 GCCCTGAACAGCCTCCGCGGCCCTCCGCCACCCCGCCAGTGTGCGGCGCGCGCGCC	604
413	Qy	CTGATGCTGCACCCCCAGCGGGG	437
605	Db	 GAGGCGCGCCCCCGGCTTCGCGCG	629

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RESULT 3
US-11-124-368A-154
; Sequence 154, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-154

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	Query Match	2.4%	Score 40.4	DB 12	Length 3320
	Best Local Similarity	53.9%	Pred. No. 1.1		
	Matches 83	Conservative 0	Mismatches 71	Indels 0	Gaps 0
Qy	713	AAATTGATGCTCATCTTCAAGAAGCTGCAGAGAGCTGTTTCAGCGTATACCCAGATCGATG	772		
Db	413	AGAACGAGATAGGCATCTCTCAAGATGGTGAAGCATCCCACTCTACAGCTGGTGGATG	472		
Qy	773	AGCTGGCCAAAGTGCACATCATCAGACACTGTGTCTTGGAGAACAGTAAAGATCTCGGACC	832		
Db	473	TGTTTGTGCCCGCAAGGAGTACTTTATCTTCTTGGAGCTGGCCACGGGGAGGAGTGT	532		
Qy	833	TTATCAGAGCATCACCGAGGACTACCACTGGA	866		
Db	533	TTGACTGGATCCTGGACCAAGGGCTACTACTCGGA	566		

RESULT 4

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US-11-124-368A-156
; Sequence 156, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 3338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-156

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	Best Local Similarity	53.9;	Pred. No. 1.1;		
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Qy	713	AAATTGATGCTCATCTTCAAGAAGCTGCAGAGCTGTTCCAGCGTACACCGATCGATG	772		
Db	413	AGAAGAGTAGGCATCTCAAGATGTTGAAGCATCCACATCTCTACAGTGGTGGATG	472		
Qy	773	AGCTGGCCAAAGTGACATCATGACACTGTGTTCTTGGAGAAACAGTAAGATCTCGGACC	832		
Db	473	TGTTTGACCCGCAAGAGTACTTTATCTTCTGGAGCTGGCCACGGGGAGGAGTGT	532		
Qy	833	TTATCAGCAGATCAACGACGACTACCACTTGGAA	866		
Db	533	TTGACTCGATCTCTGGACACCGGGCTACTACTCGGA	566		

RESULT 5
US-11-124-368A-155
; Sequence 155, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 3422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-155

	Query Match	2.4%	Score 40.4;	DB 12;	Length 3422;
	Best Local Similarity	53.9%	Pred. No. 1.1;		
	Matches 83;	Conservative 0;	Mismatches 71;	Indels 0;	Gaps 0;
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Db	413	AGAACGAGATAGGCATCTCTCAAGATGCTGAAGCATCCCAACATCTCTACAGCTGTGTGGATG	472		

773	AGCTGCCCAAGTGCA	CATCAGACACTGTGTTCTCGGAGAGACCA	CAGTAAATCTCGGACC	832
Qy				
Db				
473	TGTTTGACCCCGC	AAGGAGTACTTTATCTTCCTCGGAGCTGGCC	ACGGGAGGAGGTGT	532
Qy				
833	TTATCAGCAGCATC	ACGCGAGGACTACCACTCGA	866	
Qy				
533	TTGACTTGGATCT	CGGACGAGGCTACTACTCGGA	566	
Db				

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RESULT 6
US-09-925-065A-893863
; Sequence 893863, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 893863
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-893863

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RESULT 8
US-11-052-554A-519/c
; Sequence 519, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519
; LENGTH: 5706
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-519

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RESULT 7
US-09-925-065A-894029/c
; Sequence 894029, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24

Db 4987 CGCCGCGCGGTTGATGCGCCGCGCGGCGGTGCGCGGACCCCGCCTTGCGCCGCTT 4928
Qy 283 TGCCGGGATTCCTCCAGCGCTGTGAGCGCTGTGTGCGGGGATGACAGCC 331
Db 4927 GCGCGCGCGGAGACCGTTGCCGTCTTGGAGAGGGCGCGCTGTGCGC 4879

RESULT 9
US-11-136-527-306/c
; Sequence 306, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 306
; LENGTH: 15234
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-306

Query Match 2.2%; Score 37.8; DB 12; Length 15234;
Best Local Similarity 48.8%; Pred. No. 8.6;
Matches 102; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
Qy 162 GCCAGAGAGCATACCTTCACTCTGCTCTGCTGAGCGCGGCGCTTGAGTCCCGCCACTG 221
Db 5730 GCTGGCCAGAGTACCTTCACTCTGCTGCTGAGCGCGGCGGCTTGAGTCCCGCCACTG 5671
Qy 222 CTCGCTGCTCTGCGACCCCTGGGTGGAGTGGTGGCGGCTGCTTCTGCTTCCGCGG 281
Db 5670 GCGCTTCTGTGGTCTGCTGCTGCTGCTGCTGAGCGCGGCGGCTTCTTCTCCAGCAG 5611
Qy 282 CTCGCGGATTCCTCAGCGCTGTGAGCGCTGTGCGGGGATGAGCCCGCTGCTGTC 341
Db 5610 CTGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5551
Qy 342 TACTGAGGACTCCACTGAGGCGACTGCTG 370
Db 5550 AGCAGCGCTGCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5522

RESULT 10
US-11-096-568A-22110/c
; Sequence 22110, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22110
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1431)
; OTHER INFORMATION: Ceres Seq. ID no. 12407603
US-11-096-568A-22110

Query Match 2.2%; Score 37.6; DB 9; Length 1431;

Best Local Similarity 43.3%; Pred. No. 4.7;
Matches 175; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
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Db 1182 CTTCTCATCGCTGGCCTTCTTCTTACCTCCCGGACGACCTTGCACACAGAGCATTCG 1123
Qy 71 AGCTATGCTTGGAGACATATGATAACACACCTCAGCCCCCACCACCAAGCGCGCGACCGTA 130
Db 1122 TCTTGTTCACCGTCCGACTCCGACAGACACCTTGGCCCATGTGCTGGGCGCGCCGCTGGT 1063
Qy 131 GACGAGACCCCAAGGACCCCTGGCCACCATGGGCGCAGAGAGCATTACCTTTCATCTCTGGCT 190
Db 1062 GCCATCGTGGCAATCTTCCGCTGCTGCGACCTTGAACCGTCCCTGACATGCGGCA 1003
Qy 191 CTGCTGAGCGCGCCCTTGGAGTCCCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250
Db 1002 CAGCTTGCACGCGCGCCGCGCACAGCGCGTGTCTGCGCGGAGCGCGGAGCAGGTGAA 943
Qy 251 AGTGTGCGCGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 310
Db 942 GGTGTGTCAGTGGAACTTGAAGAGCTGCTTGGCGTGGCGACGACACCGAGGGTGTGTTT 883
Qy 311 CCTGTGTGGGGATGACGCGCCCTGCTGCTTACTGAGGACTCCACTGAGGGGACTGCTG 370
Db 882 CTTGCCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 823
Qy 371 AAGCCAACTGGGCGCAGGAGCACAATGAGTGGAGTGGCGCGCCCGCCAGCCCT 414
Db 822 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779

RESULT 11
US-10-330-773-603
; Sequence 603, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 603
; LENGTH: 38239
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-330-773-603

Query Match 2.2%; Score 37.6; DB 7; Length 38239;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 94; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
Qy 1153 GACACAGACTCGTGGGGGACCCCTTGTCTCCAGGTGTACTGTAAACCCCTGCGAGGCCCA 1212
Db 7967 GCCTGAGGCCCATCGGTAGTGGCTTTTACTGCTGATGTAGTGTAGAGAGTGGCTGCTCCC 8026
Qy 1213 GCTGCCACACCCCTTCTGGGAGAGCATGCGCTTACAGATGAGAGGGGGGACCGAACC 1272
Db 8027 CTTGCTAGCCCCCTTCCAGGTCAAAGTGGCTCCAGAGAGCGGAGGAGGGGGGAGT 8086
Qy 1273 CTTGCTGGAGAGGCTTGTAGACCTGAAGCAGTGCCTCTGCTGCTTCTCTCTCTGCTGA 1332
Db 8087 CAGTTTGTAGGAGAGACTCAGAAACTTGTGGCTCGGGGGCGGTGGACTCAGACTGA 8146
Qy 1333 CTGGGTTC 1340
Db 8147 GTGTTTCC 8154

RESULT 12


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; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-501-035-200

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Best Local Similarity 50.9%; Pred. No. 11;
Matches 88; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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Qy      390 GCACAATGGAGTGCCCCCAGCCCTGATCGTCACCCCCCAGCCGGGATGCCAGCG 449
Db      5808 GTGCACAAACCTGCCAAGGCACCTCTGCCTGTGTGCGGGGATCCAGGGCAGTGACAGG 5749

Qy      450 GCTCAAGTCAACCATGGGCGAGCAGCTTCAGCTACCCCGATGTTTAAGCTCAAAG 502
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Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Perfect score: 1713
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- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	1039	60.7	14207	8	AL356390
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9	937	54.7	111738	14	AL592304
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11	378	22.1	386	6	AX644346
12	334	19.5	393	6	AX069705
13	321	18.7	427	6	AX071660
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15	249	14.5	300	6	BD12719
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KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

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Diadexus, Inc. (US)

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Direct Submission
Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NTH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Kim Macdonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR
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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 43 Row: c Column: 17.
Location/Qualifiers

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ORIGIN

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DEFINITION Sequence 799 from Patent EP1308459.
ACCESSION AX747274
VERSION AX747274.1 GI:32131662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA: Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
1
Full-length cDNA sequences
Patent: EP 1308459-A 799 07-MAY-2003;
Helix Research Institute (JP); Research Association for
Biotechnology (JP)
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LOCUS
DEFINITION
AL356390 140207 bp DNA linear PRI 18-MAY-2005
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AL356390
ACCESSION
VERSION AL356390.24 GI:21436506
KEYWORDS HTG; DC2; FLJ12455; FLJ34633; NR0B2; NUDC; RPL12; RPL32.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Glithero, R.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
COMMENT
On Jun 17, 2002 this sequence version replaced gi:20218554.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
En: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl
RP11-344H11 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
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RESULT 7
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DEFINITION Sequence 56 from Patent WO02068633.
ACCESSION AX535029
VERSION AX535029.1 GI:25261664
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE	1	Hominidae; Homo.	
AUTHORS	Macina,R.A., Recipon,H., Chen,S.Y., Sun,Y. and Liu,C.		
TITLE	Compositions and methods relating to lung specific genes and proteins		
JOURNAL	Patent: WO 02068633-A 56 06-SEP-2002;		
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Qy	1137	ATCCTTTCAGGGCACCGACACAGACTCGTTCGGGGGCACCCCTTGCTCCAGGTGTACTGTCTA	1196
Ddb	1401	ATCCTTTCAGGGCACCGACACAGACTCGTTCGGGGGCACCCCTTGCTCCAGGTGTACTGTCTA	1460
Qy	1197	ACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAAGCATGGCTTACAGAATGAAG	1256
Ddb	1461	ACCCCTGCCAGGCCAGCTGCCACACCCCTTTCTGGGAGAAGCATGGCTTACAGAATGAAG	1520
Qy	1257	AGGGGGACAGGAACCCCTGTGGGAGAGGCTTAGACCTGAGAGAGTGCCCACTCTGGCTC	1316
Ddb	1521	AGGGGGACAGGAACCCCTGTGGGAGAGGCTTAGACCTGAGAGAGTGCCCACTCTGGCTC	1580
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Ddb	1581	CTCCTGCTTGGCTGACTGGGTTCTCTGGACCATGTGCAATTTCACTGGGGCCATGGGATCTA	1640
Qy	1377	CATCTCTTGATCCCGAGCTGGTCTGATTCCTCTGCAGGGGCCCTTCTTCTCTGCTCATG	1436
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Db 1941 TGACCACAGTTTGTAAAGTACCTCG 1964

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LOCUS AX535090 1977 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 117 from Patent WO02068633.
ACCESSION AX535090
VERSION AX535090.1 GI:25261789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Macina R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
AUTHORS Compositions and methods relating to lung specific genes and
TITLE Diadex, Inc. (US)
JOURNAL Patent: WO 02068633-A 117 06-SEP-2002;
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1103; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db 1761 CCTGACTCCATCCCTTATTCGCCACCCCTAAACCAATCATGCAAACTTCTCCCTCCCTGGGG 1820
QY 1557 TAAATCAACAGTAAAGAGCTTATCTTAATATGATTGTTGGGGGTGGGAGGGCC 1616
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QY 1677 TGACCACAGTTTGTAAAGTACCTCG 1700
Db 1941 TGACCACAGTTTGTAAAGTACCTCG 1964
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RESULT 9

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LOCUS AL592304 111738 bp DNA linear HTG 25-JUL-2001
DEFINITION Homo sapiens chromosome 1 clone RP3-426N7, 7 unordered pieces.
ACCESSION AL592304
VERSION AL592304.1 GI:14586390
KEYWORDS HTG; HTGS PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Mclay, K.
AUTHORS Direct Submission
TITLE Submitted (24-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
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COMMENT

----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dJ426N7
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 110287 bases at least Q40
Consensus quality: 110500 bases at least Q30
Consensus quality: 110681 bases at least Q20
Insert size: 111138; sum-of-contigs
Insert size: 119403; 8.4% error; agarose-fp
Quality coverage: 11.21x in Q20 bases; sum-of-contigs Quality
coverage: 10.67x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 18058: contig of 18058 bp in length
* 18059 18158: gap of 100 bp
* 18159 35144: contig of 16986 bp in length
* 35145 35244: gap of 100 bp
* 35245 54710: contig of 19466 bp in length
* 54711 54810: gap of 100 bp
* 54811 72936: contig of 18126 bp in length
* 72937 73036: gap of 100 bp
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FEATURES
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Query Match 54.7%; Score 937; DB 14; Length 111738;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1037; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 121 CGCACCCGTTAGACAGACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCATTTACCTTC 180
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Qy 181 ATCTCTGGCTCTGCTGAGCCGCGCCCTTTGAGTCCCCACCTGCTGCTCTGTGCGGACCC 240
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Qy 241 TGGGTGTGGAGTGGTCCCGGGCTGCTTCTGCTTCCGCGCTGCTCCGGGATTTGCTCCAG 300
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Qy 901 ATCATTCGCATTAGTACCCGAAAGAGCGTGTCTCGCCACAGACCTCGGAGGGTGTTCAT 960
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DEFINITION Sequence 55 from Patent WO02068633.
ACCESSION AX535028
VERSION AX535028.1 GI:25261662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to lung specific genes and proteins
JOURNAL Patent: WO 02068633-A 55 06-SEP-2002;
Diadexus, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 1.5e-211;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 104 from Patent WO02077232.
ACCESSION AX644346
VERSION AX644346.1 GI:28610405
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,
Lamson, G., Drmanac, R., Crkjenjakov, R., Drmanac, S., Dickson, M.,
Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and Strache-Crain, B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0102568-A 177 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
FEATURES
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Salceda, S., Macina, R.A., Recipon, H., Pluta, J., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to breast specific genes and proteins
JOURNAL Patent: WO 02077232-A 104 03-OCT-2002;
Diadexus, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 1.8e-207;
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ACCESSION AX069705
VERSION AX069705.1 GI:12579490
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,
Lamson, G., Drmanac, R., Crkjenjakov, R., Drmanac, S., Dickson, M.,
Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and Strache-Crain, B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0102568-A 177 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
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SOURCE Homo sapiens (human)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 728)
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.S.,
Reinhard,C., Giese,K., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V., Jones,L.W.
and Crain,B.S.
TITLE Novel human genes and gene expression products ii
JOURNAL Patent: JP 2002519000-A 4867 02-JUL-2002;
COMMENT CHIRON CORP,HYSEQ INC
OS Homo sapiens (human)
PN JP 2002519000-A/4867
PD 02-JUL-2002
PF 28-JAN-1999 JP 2000556580
PR 28-JAN-1998 US 60/072910,24-FEB-1998 US 60/075954 PR
31-MAR-1998 US 60/080114,03-APR-1998 US 60/080515 PR
03-APR-1998 US 60/080666,21-OCT-1998 US 60/105234 PR
28-OCT-1998 US 60/105877
PI LOUIS T WILLIAMS,JAIME ESCOBEDO,MICHAEL A INNIS,PABLO PI
DOMINGUEZ GARCIA,
PI JULIE SUDDUTH KLINGER,CHRISTOPH REINHARD,KLAUSE GIESE,FILIPPO
PI RANDAZZO,DAVID POT,ALTAF KASSAM,GEORGE LAMSON,RADOJE
PI DRMANAC,
PI RADOMIR CRKVENJAKOV,MARK DICKSON,SNEZANA DRMANAC,IVAN LABAT,
PI DENA LESHKOWITZ,DAVID KITA,VERONICA GARCIA,LEE WILLIAM JONES,
PI BIRJIT STACHE CRAIN
PC C12N15/09,C12N15/09,C07K14/47,C07K14/82,C07K16/18,C12N1/15, PC
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PC C12N1/21,C12N5/10,C1Q1/68,C12N15/00,C12N5/00,C12N15/00 CC n
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DEFINITION Mus musculus RIKEN cDNA 1810019J16 gene, mRNA (cDNA clone MGC:11921
IMAGE:3599314), complete cds.
ACCESSION BC006890
VERSION BC006890.1 GI:13905189
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1680)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,J., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
McKernan,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,R.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shvechenko,Y.,
Bouffard,G.G., Bialesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1680)
Direct Submission
Submitted (27-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgebcm.tmc.edu
Gumaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAK Plate: 16 Row: p Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 19526881.
FEATURES source
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/strain="FVB/N"
/db_xref="taxon:10090"
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/tissue_type="Mammary tumor; C3 (1)-Tag model. Infiltrating
ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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142..792
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/translation="MSAPSPHRAVPGGQTLRTLATMGQRVSPFSFOALNQPTSPQPA
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VCCPARTVHPHPAGMARGSPAPWAAASATMLSSKASISLTPTANPPQSLTWTTPARS
FWPSLLPHGTACLAAPSPTAPAAURSTTTPSMNRITWTLRWAVAPCRAGNSTCLFERS"
ORIGIN

Query Match 2.2%; Score 38; DB 9; Length 1680;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTTACCACCTGGATGAGCA 872
|||||
DB 885 ATCAGCAGCATCAGCAGGACTTACCACCTGGATGAGCA 922
|||||

RESULT 19
AL627228 193813 bp DNA linear ROD 04-FEB-2003
LOCUS Mouse DNA sequence from clone RP23-137L22 on chromosome 4, complete
DEFINITION sequence.
ACCESSION AL627228
VERSION AL627228.31 GI:28208155
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 193813)
Hopkins, B.
Direct Submission
Submitted (04-FEB-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 4, 2003 this sequence version replaced gi:22474404.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information
on the WormPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was finished as follows unless otherwise noted: all regions were
either double-stranded or sequenced with an alternate chemistry or
covered by high quality data (i.e., phred quality >= 30); an
attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by at least one
plasmid subclone or more than one M13 subclone; and the assembly
was confirmed by restriction digest, except on the rare occasion of
the clone being a YAC.
RP23-137L22 is from the RPCI-23 Mouse BAC Library
constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
Location/Qualifiers
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-137L22"
/clone_lib="RPCI-23"

FEATURES
source

ORIGIN

Query Match

2.2%; Score 38; DB 9; Length 193813;

Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTTACCACCTGGATGAGCA 872
|||||
DB 104723 ATCAGCAGCATCAGCAGGACTTACCACCTGGATGAGCA 104760
|||||

RESULT 20
BC079148 1718 bp mRNA linear ROD 15-SEP-2004
LOCUS Rattus norvegicus similar to hypothetical protein FLJ34633, mRNA
DEFINITION (cDNA clone MGC:94165 IMAGE:7128510), complete cds.
ACCESSION BC079148
VERSION BC079148.1 GI:50927712
KEYWORDS MGC.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
1 (bases 1 to 1718)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stepleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalley, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1718)
Director MGC Project.
Direct Submission
Submitted (02-AUG-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdepaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 184 Row: d Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, similarity but not identity to protein.

Location/Qualifiers
1..1718
/organism="Rattus norvegicus"

FEATURES

source

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/lab_host="DH10B"
/note="Vector: pExpress1"
1. 1718
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73. 1266
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GACVRSQCLSGADPTISGSEAAWKEHNGVPPSPDRAPPSRRDGOKLKTSGSSFS
YDVKLAGIPVYVRHATSPVPDADSCCKEPLADPPTRHSLPSTTSSPRGSEYVS
FHESDLDPWGSMSRSDVLLFKLTELFSVHQLDLAKTSTDTVELEKTSKLS
DLISITQDYLDDQDAEGLVRLGIIIRISTKRSRQPTSEGRSARSTAAAPDSGH
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LQVYC"

ORIGIN
Query Match 1.7%; Score 29; DB 9; Length 1718;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 994 GACAGTGCCCATGAGACCATGGTGGCTC 1022
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Db 1063 GACAGTGCCCATGAGACCATGGTGGCTC 1091

RESULT 21
AC095979
LOCUS
DEFINITION Rattus norvegicus clone CH230-11020, WORKING DRAFT SEQUENCE, 3
unordered pieces.
AC095979
VERSION AC095979.7 GI:24818145
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 235419)
Muzny,D,Marle, Metzker,M, Lee, Abramzon,S, Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Ayoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Chen,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flaggs,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregiorgis,B., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,Z., Khan,S., Khan,L., Kovar,C.,
Kowitz,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
```

```

Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,D.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokemelele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L., L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajls,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 235419)
Worley,K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235419)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:22772470.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GEBU
Center clone name: CH230-11020
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 225536 bases at least Q40
Consensus quality: 227458 bases at least Q30
Consensus quality: 228649 bases at least Q20
Estimated insert size: 235033; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
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* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 221492: contig of 221492 bp in length
 * 221493: gap of unknown length
 * 221593 228651: contig of 7059 bp in length
 * 228652 228751: gap of unknown length
 * 228752 235419: contig of 6668 bp in length.

FEATURES

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 /note="clone_boundary"
 clone_end:T7
 site:EcoRI

misc_feature

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 site:EcoRI

gap

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 end_sequence:BH344813"

gap

/estimated_length=unknown
 228652..228751
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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0.00031;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 994 GACATGCGCATGAGACCATGGTGGCTC 1022

Db 84076 GACATGCGCATGAGACCATGGTGGCTC 84104

RESULT 22

AC118963/c

LOCUS

Rattus norvegicus clone CH230-180E4, WORKING DRAFT SEQUENCE. HTG 15-NOV-2002

AC118963

DEFINITION

AC118963

ACCESSION

HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

KEYWORDS

Rattus norvegicus (Norway rat)

SOURCE

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Rattus.

1 (bases 1 to 249406)

Muzny,D,Marie,, Metzker,M, Lee,, Abramzon,S,, Adams,C,, Alder,J,,

Allen,C,, Allen,H,, Alsbrooks,S,, Amin,A,, Anguiano,D,,

Anyalebechi,V,, Aoyagi,A,, Ayodeji,M,, Baca,E,, Baden,H,,

Baldwin,D,, Bandaranaike,D,, Barber,M,, Barnstead,M,, Benahmed,F,,

Biswal,K,, Blair,J,, Blankenburg,K,, Blyth,P,, Brown,M,,

Bryant,N,, Buhay,C,, Burch,P,, Burrell,K,, Calderon,E,,

Cardenas,V,, Carter,K,, Cavazos,I,, Ceasar,H,, Center,A,,

Chacko,J,, Chavez,D,, Chen,G,, Chen,R,, Chen,Y,, Chen,Z,, Chu,J,,

Cleveland,C,, Cockrell,R,, Cox,C,, Coyle,M,, Cree,A,, D'Souza,L,,

Davila,M,L,, Davis,C,, Davy-Carroll,L,, De Anda,C,, Dederich,D,,

Delgado,O,, Denson,S,, Deramo,C,, Ding,Y,, Dinh,H,, Divya,K,,

Egan,A,, Escotto,M,, Eugene,C,, Evans,C,A,, Falls,T,, Fan,G,,

Fernandez,S,, Finley,M,, Flagg,N,, Forbes,L,, Foster,M,, Foster,P,,

Fraser,C,M,, Gabisi,A,, Ganta,R,, Garcia,A,, Garner,T,, Garza,M,,

Gebregorgis,E,, Gear,K,, Gill,R,, Grady,M,, Guerra,W,, Guevara,W,,

Gunaratne,P,, Haaland,M,, Hamil,C,, Hamilton,C,, Hamilton,K,,

Harvey,Y,, Havlak,P,, Hawes,A,, Henderson,N,, Hernandez,J,,

Hernandez,R,, Hines,S,, Hladun,S,L,, Hodgson,A,, Hogues,M,,
 Hollins,B,, Howells,S,, Hulyk,S,, Hume,J,, Idlebird,D,, Jackson,A.,
 Jackson,L,, Jacob,L,, Jiang,H,, Johnson,B,, Johnson,B,, Jolivet,A.,
 Karpachy,S,, Kelly,S,, Kelly,S,, Khan,Z,, King,L,, Kovar,C.,
 Kowis,C,, Kraft,C,L,, Lebow,H,, Levan,J,, Lewis,L,, Li,Z,, Liu,J.,
 Liu,J,, Liu,W,, Liu,Y,, London,P,, Longacre,S,, Lopez,J.,
 Lorensuhewa,L,, Loulseged,H,, Lozado,R,J,, Lu,X,, Ma,J.,
 Maheshwari,M,, Mahindaratne,M,, Mahmoud,M,, Malloy,K,, Mangum,A.,
 Mangum,B,, Mapua,P,, Martin,K,, Martin,R,, Martinez,E.,
 Mawhney,S,, McLeod,M,P,, McNeill,T,Z,, Meenen,E.,
 Milosavljevic,A,, Miner,G,, Minja,E,, Montemayor,J,, Moore,S.,
 Morgan,M,, Morris,K,, Morris,S,, Munidasa,M,, Murphy,M,, Nair,L.,
 Nankervis,C,, Neal,D,, Newton,N,, Nguyen,N,, Norris,S.,
 Nwaokemele,O,, Okwuonu,G,, Olarunpunsagoon,A,, Pal,S,, Parks,K.,
 Pasternak,S,, Paul,H,, Perez,A,, Perez,L,, Pfamkotch,C.,
 Plopper,F,, Poindestre,A,, Popovic,D,, Primus,E,, Pu,L-L.,
 Puzo,M,, Quiroz,J,, Rachlin,E,, Reeves,K,, Regier,M,A,, Reigh,R.,
 Reilly,B,, Reilly,M,, Ren,Y,, Reuter,M,, Richards,S,, Riggs,P.,
 Rives,C,, Rodkey,T,, Rojas,A,, Rose,M,, Rose,R,, Rui,S,J.,
 Sanders,W,, Savery,G,, Scherer,S,, Scott,G,, Shatman,S,, Shen,H.,
 Shetty,J,, Shvartsbeyn,A,, Sisson,I,, Sitter,C,D,, Smajs,D.,
 Sneed,A,, Sodergren,E., Song,X-Z,, Sorelle,R,, Sosa,J.,
 Steimle,M,, Strong,R,, Sutton,A,, Svatek,A,, Tabot,P,, Taylor,C.,
 Taylor,T,, Thomas,N,, Thomas,S,, Tingey,A,, Trejos,Z,, Usmani,K.,
 Valas,R,, Vera,V,, Villasana,D,, Waldron,L,, Walker,B,, Wang,J.,
 Wang,Q,, Wang,S,, Warren,J,, Warren,R,, Wei,X,, White,F.,
 Williams,G,, Willson,R,, Wleczyk,R,, Wooden,H,, Worley,K.,
 Wright,D,, Wright,R,, Wu,J,, Yakub,S,, Yen,J,, Yoon,L., Yoon,V.,
 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
 Niederhausern,A,, Weiss,R,, Smith,D,R,, Holt,R,A,, Smith,H,O.,
 Weinstock,G. and Gibbs,R.A.

Direct Submission

Unpublished

2 (bases 1 to 249406)

Worley,K.C.

Direct Submission

Submitted (22-APR-2002)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 249406)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23269749.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

in the feature table below represents a scaffold in the Atlas

assembly (a 'contig-scaffold'). Within each contig-scaffold,

individual sequence contigs are ordered and oriented, and separated

by sized gaps filled with Ns to the estimated size. The sequence

contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature

table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GVHY

Center clone name: CH230-180E4

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 213357 bases at least Q40

Consensus quality: 215358 bases at least Q30

Consensus quality: 217213 bases at least Q20

Estimated insert size: 223109; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: this is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 249406: contig of 249406 bp in length.
FEATURES
 source
 1..249406
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-180E4"
 1..1279
 /note="wgs_contig"
ORIGIN
Query Match 1.7% Score 29; DB 14; Length 249406;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 994 GACAGTGCCATGAGACCATGGTGGCTC 1022
 |||||
Db 13766 GACAGTGCCATGAGACCATGGTGGCTC 13738

RESULT 23
AC126312/c
DEFINITION Rattus norvegicus clone CH230-1B9, *** SEQUENCING IN PROGRESS ***,
 3 unordered pieces.
AC126312
AC126312.4 GI:24941465
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
REFERENCE
1 (Bases 1 to 256017)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaraturunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brlewa,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,G., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,

Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickets,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojebokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaikie,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Umani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
2 (bases 1 to 256017)
Worley,K.C.
Direct Submission
Submitted (05-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 256017)
Worley,K.C.
Direct Submission
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23267435.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: RUNJ
Center clone name: CH230-1B9
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 214827 bases at least Q40
Consensus quality: 219116 bases at least Q30
Consensus quality: 221911 bases at least Q20
Estimated insert size: 222841; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: this is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 83721: contig of 83721 bp in length
* 83722 83821: gap of unknown length
* 83822 253567: contig of 169746 bp in length
* 253568 253667: gap of unknown length
* 253668 256017: contig of 2350 bp in length.
FEATURES
 Location/Qualifiers
 1..256017
source

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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-1B9"
6668..7475
/note="clone_boundary
clone_end:17"
site:
end_sequence:BH274997"
38358..39527
/note="wgs_contig"
67950..69005
/note="wgs_contig"
78781..81213
/note="wgs_contig"
83722..83821
/estimated_length=unknown
83822..85574
/note="wgs_contig"
219978..221353
/note="wgs_contig"
253568..253667
/estimated_length=unknown

ORIGIN
Query Match 1.7%; Score 29; DB 14; Length 256017;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 GACAGTGGCCATGACACCATGGTGGGCTC 1022
Db 154754 GACAGTGGCCATGACACCATGGTGGGCTC 154726

RESULT 24
AX185505/c AX185505 323 bp DNA linear PAT 06-AUG-2001
LOCUS
DEFINITION Sequence 1200 from Patent WO0142467.
ACCESSION AX185505
VERSION AX185505.1 GI:15136902
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
AUTHORS Genes, compositions, kits, and methods for identification,
TITLE assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 1200 14-JUN-2001;
Mileennium Predictive Medicine, Inc. (US)
FEATURES
source
Location/Qualifiers
1..323
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.6%; Score 28; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 TTGTAGTACCTCGCGCGGACACGCG 1713
Db 34 TTGTAGTACCTCGCGCGGACACGCG 7

RESULT 25
AX185017/c AX185017 329 bp DNA linear PAT 06-AUG-2001
LOCUS
DEFINITION Sequence 712 from Patent WO0142467.
ACCESSION AX185017
```

```
VERSION AX185017.1 GI:15136393
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
AUTHORS Genes, compositions, kits, and methods for identification,
TITLE assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 712 14-JUN-2001;
Mileennium Predictive Medicine, Inc. (US)
FEATURES
source
Location/Qualifiers
1..329
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.6%; Score 28; DB 6; Length 329;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 TTGTAGTACCTCGCGCGGACACGCG 1713
Db 34 TTGTAGTACCTCGCGCGGACACGCG 7

RESULT 26
AX098107/c AX098107 91 bp DNA linear PAT 30-MAR-2001
LOCUS
DEFINITION Sequence 19 from Patent WO0118542.
ACCESSION AX098107
VERSION AX098107.1 GI:13514986
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Lee,J., Thompsho,P. and Lillie,J.
AUTHORS Identification, assessment, prevention, and therapy of ovarian
TITLE cancer
JOURNAL Patent: WO 0118542-A 19 15-MAR-2001;
Mileennium Predictive Medicine, Inc. (US)
FEATURES
source
Location/Qualifiers
1..91
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAGTACCTCGCGCGGACACGCG 1713
Db 32 TGTAAGTACCTCGCGCGGACACGCG 7

RESULT 27
AX185663/c AX185663 203 bp DNA linear PAT 06-AUG-2001
LOCUS
DEFINITION Sequence 1358 from Patent WO0142467.
ACCESSION AX185663
VERSION AX185663.1 GI:15137068
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
1 Hominidae; Homo.
REFERENCE
AUTHORS Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 1358 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
1..203
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAAGTACCTCGCGCGGACACGC 1713
|||||
Db 32 TGTAAGTACCTCGCGCGGACACGC 7
RESULT 28
AX186486 412 bp DNA linear PAT 06-AUG-2001
LOCUS
DEFINITION Sequence 2181 from Patent WO0142467.
ACCESSION AX186486
VERSION AX186486.1 GI:15137921
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 2181 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
1..412
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1686 TTTGTAAGTACCTCGCGCGGACAC 1711
|||||
Db 377 TTTGTAAGTACCTCGCGCGGACAC 402
RESULT 29
CQ424843 576 bp DNA linear PAT 28-JAN-2004
LOCUS
DEFINITION Sequence 9877 from Patent WO0151628.
ACCESSION CQ424843
VERSION CQ424843.1 GI:41377072
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lillie,J., Xu,Y., Wang,Y. and Steinmann,K.
TITLE Novel genes, compositions, kits, and methods for identification,

assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 9877 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1..576
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAAGTACCTCGCGCGGACACGC 1713
|||||
Db 550 TGTAAGTACCTCGCGCGGACACGC 575
RESULT 30
CQ505617/c 255 bp DNA linear PAT 30-JAN-2004
LOCUS
DEFINITION Sequence 37484 from Patent WO0160860.
ACCESSION CQ505617
VERSION CQ505617.1 GI:41471716
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 37484 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
1..255
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.5%; Score 25; DB 6; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1689 GTAAGTACCTCGCGCGGACACGC 1713
|||||
Db 97 GTAAGTACCTCGCGCGGACACGC 73
RESULT 31
CQ410339/c 275 bp DNA linear PAT 23-JAN-2004
LOCUS
DEFINITION Sequence 17410 from Patent WO0170979.
ACCESSION CQ410339
VERSION CQ410339.1 GI:41318120
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lee,J. and Lillie,J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 17410 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match      1.5%; Score 25; DB 6; Length 275;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGGACCAACGC 1713
Db 87 GTAAGTACCTCGCGCGGACCAACGC 63

RESULT 32
LOCUS      CQ475657 304 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 7524 from Patent WO0160860.
ACCESSION  CQ475657
VERSION     CQ475657.1 GI:41441276
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Schlegel, R., Endege, W.O. and Monahan, J.R.
TITLE       Genes differentially expressed in human prostate cancer and their
JOURNAL     use
FEATURES    source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

Query Match      1.5%; Score 25; DB 6; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGGACCAACGC 1713
Db 39 GTAAGTACCTCGCGCGGACCAACGC 15

RESULT 33
LOCUS      CQ398024 310 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 5095 from Patent WO0170979.
ACCESSION  CQ398024
VERSION     CQ398024.1 GI:41305805
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Lee, J. and Lillie, J.
TITLE       Genes, compositions, kits, and method for identification,
JOURNAL     assessment, prevention, and therapy of ovarian cancer
FEATURES    source
            1..310
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

Query Match      1.5%; Score 25; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGGACCAACGC 1713
Db 280 GTAAGTACCTCGCGCGGACCAACGC 304

RESULT 34
LOCUS      CQ404316 310 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 11387 from Patent WO0170979.
ACCESSION  CQ404316
VERSION     CQ404316.1 GI:41312097
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Lee, J. and Lillie, J.
TITLE       Genes, compositions, kits, and method for identification,
JOURNAL     assessment, prevention, and therapy of ovarian cancer
FEATURES    source
            1..310
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

Query Match      1.5%; Score 25; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGGACCAACGC 1713
Db 280 GTAAGTACCTCGCGCGGACCAACGC 304

RESULT 35
LOCUS      CQ421839 358 bp DNA linear PAT 28-JAN-2004
DEFINITION Sequence 6873 from Patent WO0151628.
ACCESSION  CQ421839
VERSION     CQ421839.1 GI:41374068
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
TITLE       Novel genes, compositions, kits, and methods for identification,
JOURNAL     assessment, prevention, and therapy of breast cancer
FEATURES    source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

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Query Match      1.5%; Score 25; DB 6; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAAGTACCTCGCGCGGACCAACGC 1713
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Db 31 GTAAGTACCTCGCGCGGACCACGC 7
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AX185290 359 bp DNA linear PAT 06-AUG-2001
LOCUS Sequence 985 from Patent WO0142467.
DEFINITION AX185290
ACCESSION AX185290
VERSION AX185290.1 GI:15136678
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
TITLE Genes, compositions, kits, and methods for identification,
JOURNAL assesment, prevention, and therapy of cervical cancer
PATENT: WO 0142467-A 985 14-JUN-2001; (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1689 GTAAGTACCTCGCGCGGACCACGC 1713
|||||
Db 31 GTAAGTACCTCGCGCGGACCACGC 7
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RESULT 37
CQ410700 463 bp DNA linear PAT 23-JAN-2004
LOCUS Sequence 17771 from Patent WO0170979.
DEFINITION CQ410700
ACCESSION CQ410700
VERSION CQ410700.1 GI:41318481
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
JOURNAL assesment, prevention, and therapy of ovarian cancer
PATENT: WO 0170979-A 17771 27-SEP-2001;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 1.5%; Score 25; DB 6; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1689 GTAAGTACCTCGCGCGGACCACGC 1713
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Db 351 GTAAGTACCTCGCGCGGACCACGC 375
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RESULT 38
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CS067068/c 150 bp DNA linear PAT 20-APR-2005
LOCUS Sequence 1051 from Patent WO2005030998.
DEFINITION CS067068
ACCESSION CS067068
VERSION CS067068.1 GI:62819876
KEYWORDS
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
TITLE Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
JOURNAL
REFERENCE 1
AUTHORS Berka,R., Bashkirova,E. and Rey,M.
TITLE Methods for monitoring multiple gene expression
JOURNAL Patent: WO 2005030998-A 1051 07-APR-2005;
Novozymes Biotech, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Hypocrea jecorina"
/mol_type="unassigned DNA"
/db_xref="taxon:51453"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACCTCGCGCGGACCACGC 1713
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Db 24 TAAGTACCTCGCGCGGACCACGC 1
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RESULT 39
AX718965 232 bp DNA linear PAT 15-APR-2003
LOCUS Sequence 15 from Patent WO03002599.
DEFINITION AX718965
ACCESSION AX718965
VERSION AX718965.1 GI:29891501
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
JOURNAL Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Encinas,J. and Leong,J.
TITLE Immune-related proteins and the regulation of the same
JOURNAL Patent: WO 03002599-A 15 09-JAN-2003;
Bayer Aktiengesellschaft (DE)
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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Query Match 1.4%; Score 24; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAAGTACCTCGCGCGGACCAC 1711
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Db 207 TGTAAGTACCTCGCGCGGACCAC 230
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RESULT 40
CQ410151/c 253 bp DNA linear PAT 23-JAN-2004
LOCUS Sequence 17222 from Patent WO0170979.
DEFINITION CQ410151
ACCESSION CQ410151
VERSION CQ410151.1 GI:41317932
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 1722 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
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Db 77 TAAGTACTCGCGCGACACGC 54
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RESULT 41
CQ398274/c
LOCUS CQ398274 274 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 5345 from Patent WO0170979.
ACCESSION CQ398274
VERSION CQ398274.1 GI:41306055
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 5345 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..274
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
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Db 30 TAAGTACTCGCGCGACACGC 7
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RESULT 42
CQ404561/c
LOCUS CQ404561 274 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 11632 from Patent WO0170979.
ACCESSION CQ404561
VERSION CQ404561.1 GI:41312342
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.

Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 11632 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 1.4%; Score 24; DB 6; Length 274;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
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Db 30 TAAGTACTCGCGCGACACGC 7
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RESULT 43
CQ409324/c
LOCUS CQ409324 283 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 16395 from Patent WO0170979.
ACCESSION CQ409324
VERSION CQ409324.1 GI:41317105
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 16395 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 1.4%; Score 24; DB 6; Length 283;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
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Db 54 TAAGTACTCGCGCGACACGC 31
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RESULT 44
CQ396607/c
LOCUS CQ396607 310 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 3678 from Patent WO0170979.
ACCESSION CQ396607
VERSION CQ396607.1 GI:41304388
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 3678 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers

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/mol_type="unassigned DNA"
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 45
LOCUS CQ402920/c 310 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 9991 from Patent WO0170979.
ACCESSION CQ402920
VERSION CQ402920.1 GI:41310701
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 991 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 100.0%; Score 24; DB 6; Length 310;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 46
LOCUS CQ397003/c 312 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 4074 from Patent WO0170979.
ACCESSION CQ397003
VERSION CQ397003.1 GI:41304784
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 4074 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Qy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 47
LOCUS CQ403310 312 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 10381 from Patent WO0170979.
ACCESSION CQ403310
VERSION CQ403310.1 GI:41311091
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 10381 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 48
LOCUS CQ395905 319 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 2976 from Patent WO0170979.
ACCESSION CQ395905
VERSION CQ395905.1 GI:41303686
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 2976 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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/db_xref="taxon:9606"

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Best Local Similarity 100.0%; Score 24; DB 6; Length 319;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1690 TAAGTACCTCGCGCGGACCGC 1713
LOCUS
Db 30 TAAGTACCTCGCGCGGACCGC 7

RESULT 49
CQ402234/c
LOCUS
DEFINITION Sequence 9305 from Patent WO0170979. linear PAT 23-JAN-2004
ACCESSION CQ402234
VERSION CQ402234.1 GI:41310015
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 9305 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCGC 1713
Db 30 TAAGTACCTCGCGCGGACCGC 7

RESULT 50
CQ410876/c
LOCUS
DEFINITION Sequence 17947 from Patent WO0170979. linear PAT 23-JAN-2004
ACCESSION CQ410876
VERSION CQ410876.1 GI:41318657
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 17947 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 326;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCGC 1713
Db 113 TAAGTACCTCGCGCGGACCGC 90

RESULT 51
AX185234/c
LOCUS
DEFINITION Sequence 929 from Patent WO0142467. linear PAT 06-AUG-2001
ACCESSION AX185234
VERSION AX185234.1 GI:15136619
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
TITLE Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 929 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCGC 1713
Db 30 TAAGTACCTCGCGCGGACCGC 7

RESULT 52
CQ420511/c
LOCUS
DEFINITION Sequence 5545 from Patent WO0151628. linear PAT 28-JAN-2004
ACCESSION CQ420511
VERSION CQ420511.1 GI:41372740
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
TITLE Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer
JOURNAL Patent: WO 0151628-A 5545 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCGC 1713
Db 30 TAAGTACCTCGCGCGGACCGC 7

RESULT 53
AX185287/c
LOCUS
DEFINITION Sequence 982 from Patent WO0142467. linear PAT 06-AUG-2001
ACCESSION AX185287

VERSION AX185287.1 GI:15136675
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 982 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 338;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGACACGC 1713
Db 30 TAAGTACTCGCGCGACACGC 7
RESULT 54
LOCUS CQ476128/ 346 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 7995 from Patent WO0160860.
ACCESSION CQ476128
VERSION CQ476128.1 GI:41441747
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 7995 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES source
Location/Qualifiers
1..346
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 346;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGACACGC 1713
Db 30 TAAGTACTCGCGCGACACGC 7
RESULT 55
LOCUS CQ397640/ 368 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 4711 from Patent WO0170979.
ACCESSION CQ397640
VERSION CQ397640.1 GI:41305421
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 4711 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.4%; Score 24; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGACACGC 1713
Db 30 TAAGTACTCGCGCGACACGC 7
RESULT 56
LOCUS CQ403939/ 368 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 11010 from Patent WO0170979.
ACCESSION CQ403939
VERSION CQ403939.1 GI:41311720
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 11010 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 1.4%; Score 24; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGACACGC 1713
Db 30 TAAGTACTCGCGCGACACGC 7
RESULT 57
LOCUS CQ398887/ 370 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 5958 from Patent WO0170979.
ACCESSION CQ398887
VERSION CQ398887.1 GI:41306668
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,

QY 1850 TAAAGTACCTCGGCCCGACACGC 7

RESULT 60
CQ409694/c
LOCUS CQ409694 382 bp DNA linear
DEFINITION Sequence 16765 from Patent WO0170979.
PAT 23-JAN-2004

ACCESSION	CQ403634
VERSION	CQ403634.1
KEYWORDS	GI:41317475
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homidae; Homininae; Homo.
REFERENCE	1

Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 16765 27-SEP-2001;
JOURNAL

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RESULT 61				
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LOCUS	CQ395831	391 bp	DNA	linear
				PAT 23-JAN-2004

ACCESSION	CQ395831	
VERSION	CQ395831.1	GI:41303612
KEYWORDS	.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	

REFERENCE
AUTHORS
TITLE
JOURNAL

1 Lee, J. and Lillie, J.
Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 2902 27-SEP-2001;

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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 62
LOCUS CQ402160 391 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 9231 from Patent WO0170979.
ACCESSION CQ402160
VERSION CQ402160.1 GI:41309941
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 9231 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 63
LOCUS CQ409304 391 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 16375 from Patent WO0170979.
ACCESSION CQ409304
VERSION CQ409304.1 GI:41317085
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 16375 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713

Db 110 TAAGTACTCGCGCGGACACGC 87

RESULT 64
LOCUS CQ396196 392 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 3267 from Patent WO0170979.
ACCESSION CQ396196
VERSION CQ396196.1 GI:41303977
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 3267 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 65
LOCUS CQ402521 392 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 9592 from Patent WO0170979.
ACCESSION CQ402521
VERSION CQ402521.1 GI:41310302
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 9592 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713
Db 30 TAAGTACTCGCGCGGACACGC 7

RESULT 66

CQ476176/c
LOCUS CQ476176 404 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 8043 from Patent WO0160860.
ACCESSION CQ476176
VERSION CQ476176.1 GI:41441795
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Schlegel, R., Endege, W.O. and Monahan, J.E.
JOURNAL Genes differentially expressed in human prostate cancer and their
FEATURES use
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTGGCGCGACACGC 1713
Db 30 TAAGTACTCTGGCGCGACACGC 7
RESULT 67
CQ408978/c
LOCUS CQ408978 409 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 16049 from Patent WO0170979.
ACCESSION CQ408978
VERSION CQ408978.1 GI:41316759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Lee, J. and Lillie, J.
JOURNAL Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 16049 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTGGCGCGACACGC 1713
Db 111 TAAGTACTCTGGCGCGACACGC 88
RESULT 68
CQ410088/c
LOCUS CQ410088 415 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 17159 from Patent WO0170979.
ACCESSION CQ410088
VERSION CQ410088.1 GI:41317869

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Lee, J. and Lillie, J.
JOURNAL Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 17159 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 1.4%; Score 24; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTGGCGCGACACGC 1713
Db 111 TAAGTACTCTGGCGCGACACGC 88
RESULT 69
CQ398150/c
LOCUS CQ398150 416 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 5221 from Patent WO0170979.
ACCESSION CQ398150
VERSION CQ398150.1 GI:41305931
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Lee, J. and Lillie, J.
JOURNAL Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
Patent: WO 0170979-A 5221 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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QY 1690 TAAGTACTCTGGCGCGACACGC 1713
Db 30 TAAGTACTCTGGCGCGACACGC 7
RESULT 70
CQ404437/c
LOCUS CQ404437 416 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 11508 from Patent WO0170979.
ACCESSION CQ404437
VERSION CQ404437.1 GI:41312218
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 11508 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACCTCGCGCGGACCAACGC 1713
Db 30 TAAGTACCTCGCGCGGACCAACGC 7
RESULT 71
LOCUS CQ405708 420 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 12779 from Patent WO0170979.
ACCESSION CQ405708
VERSION CQ405708.1 GI:41313489
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 12779 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACCTCGCGCGGACCAACGC 1713
Db 391 TAAGTACCTCGCGCGGACCAACGC 414
RESULT 72
LOCUS CQ408618 420 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 15689 from Patent WO0170979.
ACCESSION CQ408618
VERSION CQ408618.1 GI:41316399
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer

JOURNAL Patent: WO 0170979-A 15689 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Qy 1690 TAAGTACCTCGCGCGGACCAACGC 1713
Db 111 TAAGTACCTCGCGCGGACCAACGC 88
RESULT 73
LOCUS CQ398742 421 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 5813 from Patent WO0170979.
ACCESSION CQ398742
VERSION CQ398742.1 GI:41306523
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 5813 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACCTCGCGCGGACCAACGC 1713
Db 391 TAAGTACCTCGCGCGGACCAACGC 414
RESULT 74
LOCUS CQ507382 424 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 39249 from Patent WO0160860.
ACCESSION CQ507382
VERSION CQ507382.1 GI:41473592
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 39249 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES Location/Qualifiers
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Qy 1690 TAAGTACTCTCGCGCGGACCGC 1713
Db 85 TAAGTACTCTCGCGCGGACCGC 62

RESULT 75
CQ411425/c
LOCUS CQ411425 426 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 18496 from Patent WO0170979.
ACCESSION CQ411425
VERSION CQ411425.1 GI:41319206
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1 Lee, J. and Lillie, J.
  Genes, compositions, kits, and method for identification,
  assessment, prevention, and therapy of ovarian cancer
  Patent: WO 0170979-A 18496 27-SEP-2001;
  Millennium Pharmaceuticals, Inc. (US)
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTCGCGCGGACCGC 1713
Db 111 TAAGTACTCTCGCGCGGACCGC 88

RESULT 76
CQ474699/c
LOCUS CQ474699 426 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6566 from Patent WO0160860.
ACCESSION CQ474699
VERSION CQ474699.1 GI:41440318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1 Schlegel, R., Endege, W.O. and Monahan, J.E.
  Genes differentially expressed in human prostate cancer and their
  use
  Patent: WO 0160860-A 6566 23-AUG-2001;
  Millennium Predictive Medicine, Inc. (US)
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTCGCGCGGACCGC 1713
Db 111 TAAGTACTCTCGCGCGGACCGC 88

RESULT 76
CQ474699/c
LOCUS CQ474699 426 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6566 from Patent WO0160860.
ACCESSION CQ474699
VERSION CQ474699.1 GI:41440318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1 Schlegel, R., Endege, W.O. and Monahan, J.E.
  Genes differentially expressed in human prostate cancer and their
  use
  Patent: WO 0160860-A 6566 23-AUG-2001;
  Millennium Predictive Medicine, Inc. (US)
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTCGCGCGGACCGC 1713
Db 111 TAAGTACTCTCGCGCGGACCGC 88

RESULT 76
CQ474699/c
LOCUS CQ474699 426 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6566 from Patent WO0160860.
ACCESSION CQ474699
VERSION CQ474699.1 GI:41440318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1 Schlegel, R., Endege, W.O. and Monahan, J.E.
  Genes differentially expressed in human prostate cancer and their
  use
  Patent: WO 0160860-A 6566 23-AUG-2001;
  Millennium Predictive Medicine, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTCGCGCGGACCGC 1713
Db 95 TAAGTACTCTCGCGCGGACCGC 72

RESULT 77
CQ411551/c
LOCUS CQ411551 432 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 18622 from Patent WO0170979.
ACCESSION CQ411551
VERSION CQ411551.1 GI:41319332
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1 Lee, J. and Lillie, J.
  Genes, compositions, kits, and method for identification,
  assessment, prevention, and therapy of ovarian cancer
  Patent: WO 0170979-A 18622 27-SEP-2001;
  Millennium Pharmaceuticals, Inc. (US)
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTCGCGCGGACCGC 1713
Db 95 TAAGTACTCTCGCGCGGACCGC 72

RESULT 78
CQ506077/c
LOCUS CQ506077 432 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 37944 from Patent WO0160860.
ACCESSION CQ506077
VERSION CQ506077.1 GI:41472201
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  1 Schlegel, R., Endege, W.O. and Monahan, J.E.
  Genes differentially expressed in human prostate cancer and their
  use
  Patent: WO 0160860-A 37944 23-AUG-2001;
  Millennium Predictive Medicine, Inc. (US)
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

ORIGIN
Query Match
  1.4%; Score 24; DB 6; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTCGCGCGGACCGC 1713
Db 95 TAAGTACTCTCGCGCGGACCGC 72
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Db          56 TAAGTACTCGCGCGACACGC 33
LOCUS
DEFINITION Sequence 3100 from Patent WO0170979.
ACCESSION CQ396029
VERSION CQ396029.1 GI:41303810
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
          Lee, J. and Lillie, J.
          Genes, compositions, kits, and method for identification,
          assessment, prevention, and therapy of ovarian cancer
          Patent: WO 0170979-A 3100 27-SEP-2001;
          Millennium Pharmaceuticals, Inc. (US)
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              /mol_type="unassigned DNA"
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Query Match      1.4%; Score 24; DB 6; Length 437;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
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Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 80
LOCUS
DEFINITION Sequence 9426 from Patent WO0170979.
ACCESSION CQ402355
VERSION CQ402355.1 GI:41310136
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
          Lee, J. and Lillie, J.
          Genes, compositions, kits, and method for identification,
          assessment, prevention, and therapy of ovarian cancer
          Patent: WO 0170979-A 9426 27-SEP-2001;
          Millennium Pharmaceuticals, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
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Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 81
LOCUS
DEFINITION Sequence 4306 from Patent WO0170979.
ACCESSION CQ397235
VERSION CQ397235.1 GI:41305016
KEYWORDS
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LOCUS
DEFINITION Sequence 18016 from Patent WO0170979.
ACCESSION CQ410945
VERSION CQ410945.1 GI:41318726
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
          Lee, J. and Lillie, J.
          Genes, compositions, kits, and method for identification,
          assessment, prevention, and therapy of ovarian cancer
          Patent: WO 0170979-A 18016 27-SEP-2001;
          Millennium Pharmaceuticals, Inc. (US)
FEATURES
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              /mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
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Db 106 TAAGTACTCGCGCGACACGC 83

RESULT 82
LOCUS
DEFINITION Sequence 15845 from Patent WO0170979.
ACCESSION CQ408774
VERSION CQ408774.1 GI:41316555
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
          Lee, J. and Lillie, J.
          Genes, compositions, kits, and method for identification,
          assessment, prevention, and therapy of ovarian cancer
          Patent: WO 0170979-A 15845 27-SEP-2001;
          Millennium Pharmaceuticals, Inc. (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 73 TAAGTACTCGCGCGACACGC 50

RESULT 83
LOCUS
DEFINITION Sequence 446 bp
ACCESSION CQ397235
VERSION CQ397235.1 GI:41305016
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 4306 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 1..446 Score 24; DB 6; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7
RESULT 84
CO403539/c
LOCUS CQ403539 446 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 10610 from Patent WO0170979.
ACCESSION CQ403539
VERSION CQ403539.1 GI:41311320
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 10610 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7
RESULT 85
CO504192/c
LOCUS CQ504192 446 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 36059 from Patent WO0160860.
ACCESSION CQ504192
VERSION CQ504192.1 GI:41470221
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 36059 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES Location/Qualifiers
source
1..446
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 1..446 Score 24; DB 6; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 101 TAAGTACCTCGCGCGGACACGC 78
RESULT 86
CO506124/c
LOCUS CQ506124 446 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 37991 from Patent WO0160860.
ACCESSION CQ506124
VERSION CQ506124.1 GI:41472250
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 37991 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 1..446 Score 24; DB 6; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 71 TAAGTACCTCGCGCGGACACGC 48
RESULT 87
CO513253/c
LOCUS CQ513253 446 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 45120 from Patent WO0160860.
ACCESSION CQ513253
VERSION CQ513253.1 GI:41479517
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 45120 23-AUG-2001;

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FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.22; Mismatches 0; Indels 0; Gaps 0;
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Qy 1690 TAAGTACCTCGCGCGGACACGCG 1713
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Db 101 TAAGTACCTCGCGCGGACACGCG 78

RESULT 88
LOCUS KPN293850/c 450 bp DNA linear BCT 24-NOV-2000
DEFINITION Klebsiella pneumoniae partial EVGA gene for putative positive
transcription regulator EVGA, contig region pSL042.
ACCESSION AJ293850
VERSION AJ293850.1 GI:9909726
KEYWORDS EVGA gene; positive transcription regulator EVGA.
SOURCE Klebsiella pneumoniae
ORGANISM Klebsiella pneumoniae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
REFERENCE 1
AUTHORS Lai, Y.C., Yang, S.L., Peng, H.L. and Chang, H.Y.
TITLE Identification of genes present specifically in a virulent strain
of Klebsiella pneumoniae
JOURNAL Infect. Immun. 68 (12), 7149-7151 (2000)
PUBMED 11083844
REFERENCE 2 (bases 1 to 450)
AUTHORS Yang, S.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Yang S., Life Science, National Tsing Hua
University, 101, Section 2 Kuang Fu Road, Hsinchu, 300, TAIWAN
FEATURES
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    /db_xref="taxon:573"
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Qy 1690 TAAGTACCTCGCGCGGACACGCG 1713
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Db 101 TAAGTACCTCGCGCGGACACGCG 78

RESULT 89
LOCUS AX523478/c 457 bp DNA linear PAT 24-OCT-2002
DEFINITION Sequence 66 from Patent WO02064788.
ACCESSION AX523478
VERSION AX523478.1 GI:24412374
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to lung specific genes and
proteins
JOURNAL Patent: WO 02064788-A 66 22-AUG-2002;
Diadexus, Inc. (US)
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Qy 1690 TAAGTACCTCGCGCGGACACGCG 1713
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RESULT 90
LOCUS CQ411634/c 460 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 18705 from Patent WO0170979.
ACCESSION CQ411634
VERSION CQ411634.1 GI:41319415
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 18705 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.22; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACCTCGCGCGGACACGCG 1713
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Db 108 TAAGTACCTCGCGCGGACACGCG 85

RESULT 91
LOCUS CQ396273/c 464 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 3344 from Patent WO0170979.
Qy 1690 TAAGTACCTCGCGCGGACACGCG 1713
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Db 108 TAAGTACCTCGCGCGGACACGCG 85
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ACCESSION CQ396273
VERSION CQ396273.1 GI:41304054
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 3344 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 1.4%; Score 24; DB 6; Length 464;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGGACCAAGC 1713
Db 30 TAAGTACTCGCGCGGACCAAGC 7
RESULT 92
CQ402594/c
LOCUS CQ402594 464 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 9665 from Patent WO0170979.
ACCESSION CQ402594
VERSION CQ402594.1 GI:41310375
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 9665 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 30 TAAGTACTCGCGCGGACCAAGC 7
RESULT 93
CQ408780/c
LOCUS CQ408780 471 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 15851 from Patent WO0170979.
ACCESSION CQ408780
VERSION CQ408780.1 GI:41316561
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 9665 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGGACCAAGC 1713
Db 30 TAAGTACTCGCGCGGACCAAGC 7
RESULT 94
CQ397401/c
LOCUS CQ397401 486 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 4472 from Patent WO0170979.
ACCESSION CQ397401
VERSION CQ397401.1 GI:41305182
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 4472 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGGACCAAGC 1713
Db 30 TAAGTACTCGCGCGGACCAAGC 7
RESULT 95
CQ403704/c
LOCUS CQ403704 486 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 10775 from Patent WO0170979.
ACCESSION CQ403704
VERSION CQ403704.1 GI:41311485
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Lee, J. and Lillie, J.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 15851 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
1. .471
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACTCGCGCGGACCAAGC 1713
Db 103 TAAGTACTCGCGCGGACCAAGC 80
RESULT 94
CQ397401/c
LOCUS CQ397401 486 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 4472 from Patent WO0170979.
ACCESSION CQ397401
VERSION CQ397401.1 GI:41305182
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 4472 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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ACCESSION CQ403704
VERSION CQ403704.1 GI:41311485
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Lee, J. and Lillie, J.

TITLE	Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL	Patent: WO 0170979-A 10775 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
FEATURES	Location/Qualifiers
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DEFINITION	Sequence 836 from Patent WO0142467.
ACCESSION	AX185141
VERSION	AX185141.1 GI:15136522
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
TITLE	Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer
JOURNAL	Patent: WO 0142467-A 836 14-JUN-2001; Millennium Predictive Medicine, Inc. (US)
FEATURES	Location/Qualifiers
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LOCUS	CQ409296
DEFINITION	Sequence 16367 from Patent WO0170979.
ACCESSION	CQ409296
VERSION	CQ409296.1 GI:41317077
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Lee,J. and Lillie,J.
TITLE	Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL	Patent: WO 0170979-A 16367 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
FEATURES	Location/Qualifiers
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ACCESSION	CQ397922
VERSION	CQ397922.1 GI:41305703
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Lee,J. and Lillie,J.
TITLE	Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL	Patent: WO 0170979-A 4993 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
FEATURES	Location/Qualifiers
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TITLE	Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL	Patent: WO 0170979-A 10775 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
FEATURES	Location/Qualifiers
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LOCUS	CQ408905
DEFINITION	Sequence 15976 from Patent WO0170979.
ACCESSION	CQ408905
VERSION	CQ408905.1 GI:41316686
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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Lee,J. and Lillie,J.
TITLE	Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL	Patent: WO 0170979-A 15976 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
FEATURES	Location/Qualifiers
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TITLE	Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer
JOURNAL	Patent: WO 0170979-A 15976 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
FEATURES	Location/Qualifiers
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 DEFINITION Sequence 11286 from Patent WO0170979.

ACCESSION CQ404215
 VERSION CQ404215.1 GI:41311996

KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1
 AUTHORS Lee, J. and Lillie, J.
 TITLE Genes, compositions, kits, and method for identification,
 assessment, prevention, and therapy of ovarian cancer
 JOURNAL Patent: WO 0170979-A 11286 27-SEP-2001;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES
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OM nucleic - nucleic search, using sw model

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SUMMARIES

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7	385	22.5	385	6	ABX92013
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11	321	18.7	427	5	AAF66376
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C 95	24	1.4	486	5	ADI71730	Adi71730 Human ova	C 168	23	1.3	142	5	ADL37078	Adl37078 Human ova
C 96	24	1.4	500	4	AAH69562	Aah69562 Human cer	C 169	23	1.3	143	5	ADL44859	Adl44859 Human ova
C 97	24	1.4	503	5	ADL42477	Adl42477 Human ova	C 170	23	1.3	147	5	ADL37494	Adl37494 Human ova
C 98	24	1.4	517	5	ADL42086	Adl42086 Human ova	C 171	23	1.3	147	5	ADI72350	Adi72350 Human ova
C 99	24	1.4	521	5	ADI72251	Adi72251 Human ova	C 172	23	1.3	147	14	ADY99160	Ady99160 T reesei
C 100	24	1.4	521	5	ADL41725	Adl41725 Human ova	C 173	23	1.3	149	5	ABV07432	Abv07432 Human pro
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C 102	24	1.4	524	4	AAH69765	Aah69765 Human cer	C 175	23	1.3	149	5	ADI72787	Adi72787 Human ova
C 103	24	1.4	524	5	ADL44002	Adl44002 Human ova	C 176	23	1.3	150	5	ABV37344	Abv37344 Human pro
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C 105	24	1.4	534	5	ADL38215	Adl38215 Human ova	C 178	23	1.3	151	5	ADL38426	Adl38426 Human ova
C 106	24	1.4	534	5	ADI73081	Adi73081 Human ova	C 179	23	1.3	151	5	ADI73295	Adi73295 Human ova
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C 109	24	1.4	548	5	ADL38431	Adl38431 Human ova	C 182	23	1.3	156	5	ADL37417	Adl37417 Human ova
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C 127	24	1.4	818	6	ABQ66927	Abq66927 Human exp	C 200	23	1.3	172	5	ADL38611	Adl38611 Human ova
C 128	24	1.4	872	11	ACN83198	Acn83198 Breast ca	C 201	23	1.3	172	5	ADI73481	Adi73481 Human ova
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C 135	23	1.3	54	4	AAH07761	Aah07761 Cervical	C 208	23	1.3	177	5	ABV35931	Abv35931 Human pro
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C 138	23	1.3	82	5	AAH98632	Aah98632 Human ova	C 211	23	1.3	177	5	ADL44790	Adl44790 Human ova
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C 141	23	1.3	88	5	ADL45036	Adl45036 Human ova	C 214	23	1.3	177	14	ADY99639	Ady99639 T reesei
C 142	23	1.3	92	4	AAH07811	Aah07811 Cervical	C 215	23	1.3	178	5	ABV08201	Abv08201 Human pro
C 143	23	1.3	92	5	ADL44388	Adl44388 Human ova	C 216	23	1.3	178	5	ADL38728	Adl38728 Human ova
C 144	23	1.3	94	14	ADY99584	Ady99584 T reesei	C 217	23	1.3	178	5	ADI73598	Adi73598 Human ova
C 145	23	1.3	96	5	ADL44706	Adl44706 Human ova	C 218	23	1.3	179	4	AAH70006	Aah70006 Human cer
C 146	23	1.3	103	5	ABV07864	Abv07864 Human pro	C 219	23	1.3	179	5	ADI72023	Adi72023 Human ova
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C 150	23	1.3	115	5	ABH11124	Abh11124 Human ner	C 223	23	1.3	181	5	ABV38094	Abv38094 Human pro
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C 152	23	1.3	117	14	ADY99491	Ady99491 T reesei	C 225	23	1.3	183	5	ADI71856	Adi71856 Human ova
C 153	23	1.3	119	4	AAH07746	Aah07746 Cervical	C 226	23	1.3	183	5	ADL37007	Adl37007 Human ova
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C 156	23	1.3	122	10	ABT22949	Abt22949 Breast ca	C 229	23	1.3	187	5	ABV07994	Abv07994 Human pro
C 157	23	1.3	127	5	ADL38453	Adl38453 Human ova	C 230	23	1.3	187	5	ABV37710	Abv37710 Human pro
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C 162	23	1.3	133	5	ADI72651	Adi72651 Human ova	C 235	23	1.3	189	4	AAH15994	Aah15994 Human bre
C 163	23	1.3	133	5	ADL37790	Adl37790 Human ova	C 236	23	1.3	189	5	ADL42273	Adl42273 Human ova
C 164	23	1.3	136	5	ABV07461	Abv07461 Human pro	C 237	23	1.3	190	5	ABV37682	Abv37682 Human pro
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C 242	23	1.3	193	5	ABV37615	Abv37615 Human pro	C 315	23	1.3	246	5	ADI72681	Adi72681 Human ova
C 243	23	1.3	194	4	AAH70137	Aah70137 Human cer	C 316	23	1.3	246	5	ADL37820	Adl37820 Human ova
C 244	23	1.3	195	5	ABV37466	Abv37466 Human pro	C 317	23	1.3	247	5	ADL44864	Adl44864 Human ova
C 245	23	1.3	195	5	ADI73063	Adi73063 Human ova	C 318	23	1.3	247	14	ADY99362	Ady99362 T_reesei
C 246	23	1.3	195	5	ADI38198	Adi38198 Human ova	C 319	23	1.3	248	5	ADI72316	Adi72316 Human ova
C 247	23	1.3	195	5	ADL44837	Adl44837 Human ova	C 320	23	1.3	248	5	ADL44051	Adl44051 Human ova
C 248	23	1.3	196	5	ABV36903	Abv36903 Human pro	C 321	23	1.3	248	5	ADL37460	Adl37460 Human ova
C 249	23	1.3	196	5	ABV38080	Abv38080 Human pro	C 322	23	1.3	249	5	ADI73073	Adi73073 Human ova
C 250	23	1.3	198	4	AA507727	Aas07727 Cervical	C 323	23	1.3	249	5	ADL38207	Adl38207 Human ova
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C 252	23	1.3	198	5	ADI37209	Adi37209 Human ova	C 325	23	1.3	250	5	ADI70589	Adi70589 Human ova
C 253	23	1.3	200	5	ABV08135	Abv08135 Human pro	C 326	23	1.3	250	14	ADY99318	Ady99318 T_reesei
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C 255	23	1.3	200	5	ADI73523	Adi73523 Human ova	C 328	23	1.3	252	5	ABV38113	Abv38113 Human pro
C 256	23	1.3	203	5	ADL44849	Adl44849 Human ova	C 329	23	1.3	253	5	ABV08181	Abv08181 Human pro
C 257	23	1.3	203	5	ADI37929	Adi37929 Human ova	C 330	23	1.3	253	5	ADI72143	Adi72143 Human ova
C 258	23	1.3	203	5	ADL44881	Adl44881 Human ova	C 331	23	1.3	253	5	ADL37667	Adl37667 Human ova
C 259	23	1.3	203	5	ADI72790	Adi72790 Human ova	C 332	23	1.3	253	5	ADI72528	Adi72528 Human ova
C 260	23	1.3	205	5	ADL44359	Adl44359 Human ova	C 333	23	1.3	253	5	ADL37291	Adl37291 Human ova
C 261	23	1.3	206	4	ADL44537	Adl44537 Human ova	C 334	23	1.3	254	4	AAH70098	Aah70098 Human cer
C 262	23	1.3	207	4	AA507749	Aas07749 Cervical	C 335	23	1.3	254	4	AAH69930	Aah69930 Human cer
C 263	23	1.3	207	5	ABV07950	Abv07950 Human pro	C 336	23	1.3	254	5	ABV35993	Abv35993 Human pro
C 264	23	1.3	209	5	ABV07955	Abv07955 Human pro	C 337	23	1.3	255	5	AAH82158	Aah82158 Rat diffe
C 265	23	1.3	209	5	ADI38659	Adi38659 Human ova	C 338	23	1.3	255	5	AAH82061	Aah82061 Rat diffe
C 266	23	1.3	209	5	ADI73529	Adi73529 Human ova	C 339	23	1.3	255	5	ABV37771	Abv37771 Human pro
C 267	23	1.3	209	5	ADI77177	Adi77177 Human ova	C 340	23	1.3	257	4	AAH70066	Aah70066 Human cer
C 268	23	1.3	209	5	ADI70863	Adi70863 Human ova	C 341	23	1.3	257	4	AAH70073	Aah70073 Human cer
C 269	23	1.3	210	5	ADL44810	Adl44810 Human ova	C 342	23	1.3	257	5	ABV35942	Abv35942 Human pro
C 270	23	1.3	211	5	ABV37395	Abv37395 Human pro	C 343	23	1.3	257	5	ADL44735	Adl44735 Human ova
C 271	23	1.3	211	5	ABV08226	Abv08226 Human pro	C 344	23	1.3	257	12	ADP83360	Adp83360 Breast sp
C 272	23	1.3	212	4	AAH69501	Aah69501 Human cer	C 345	23	1.3	258	5	ABV37311	Abv37311 Human pro
C 273	23	1.3	212	10	ABT23044	Abt23044 Breast ca	C 346	23	1.3	258	5	ADI71975	Adi71975 Human ova
C 274	23	1.3	212	14	ADY99604	Ady99604 T_reesei	C 347	23	1.3	258	5	ADI72518	Adi72518 Human ova
C 275	23	1.3	213	5	ADL44591	Adl44591 Human ova	C 348	23	1.3	258	5	ADI72518	Adi72518 Human ova
C 276	23	1.3	214	5	ABV38022	Abv38022 Human pro	C 349	23	1.3	258	5	ADL37125	Adl37125 Human ova
C 277	23	1.3	217	5	ABV07377	Abv07377 Human pro	C 350	23	1.3	258	5	ADL37657	Adl37657 Human ova
C 278	23	1.3	219	4	AAH69486	Aah69486 Human cer	C 351	23	1.3	259	5	ABV37617	Abv37617 Human pro
C 279	23	1.3	220	5	ABV07337	Abv07337 Human pro	C 352	23	1.3	259	14	ADY99605	Ady99605 T_reesei
C 280	23	1.3	221	5	ADL44311	Adl44311 Human ova	C 353	23	1.3	260	4	AA113303	Aal13303 Human bre
C 281	23	1.3	222	5	ADL44838	Adl44838 Human ova	C 354	23	1.3	260	5	ABV37366	Abv37366 Human pro
C 282	23	1.3	222	5	ADL44460	Adl44460 Human ova	C 355	23	1.3	260	5	ADL37961	Adl37961 Human ova
C 283	23	1.3	224	4	AAH69963	Aah69963 Human cer	C 356	23	1.3	260	5	ADI72822	Adi72822 Human ova
C 284	23	1.3	224	4	AAH69929	Aah69929 Human cer	C 357	23	1.3	260	12	ADL00209	Adl00209 Malignant
C 285	23	1.3	224	4	AAH69731	Aah69731 Human cer	C 358	23	1.3	261	5	ADI71099	Adi71099 Human ova
C 286	23	1.3	225	4	AAH70076	Aah70076 Human cer	C 359	23	1.3	261	5	ADL36260	Adl36260 Human ova
C 287	23	1.3	225	5	AAH98622	Aah98622 Human ova	C 360	23	1.3	263	5	ADI71894	Adi71894 Human ova
C 288	23	1.3	226	5	ADI72788	Adi72788 Human ova	C 361	23	1.3	263	5	ADL37045	Adl37045 Human ova
C 289	23	1.3	226	5	ADI73727	Adi73727 Human ova	C 362	23	1.3	264	4	AA114372	Aal14372 Human bre
C 290	23	1.3	227	5	ABV07996	Abv07996 Human pro	C 363	23	1.3	264	5	ADL38218	Adl38218 Human ova
C 291	23	1.3	227	5	ADI73299	Adi73299 Human ova	C 364	23	1.3	264	5	ADI72366	Adi72366 Human ova
C 292	23	1.3	227	5	ADL38430	Adl38430 Human ova	C 365	23	1.3	264	5	ADI73084	Adi73084 Human ova
C 293	23	1.3	227	10	ABT22865	Abt22865 Breast ca	C 366	23	1.3	264	5	ADL37510	Adl37510 Human ova
C 294	23	1.3	231	5	ADL44202	Adl44202 Human ova	C 367	23	1.3	265	5	AAH98667	Aah98667 Human ova
C 295	23	1.3	232	5	ABV37391	Abv37391 Human pro	C 368	23	1.3	266	5	ABV36040	Abv36040 Human pro
C 296	23	1.3	234	5	ADL43326	Adl43326 Human ova	C 369	23	1.3	266	5	ABV45100	Abv45100 Human pro
C 297	23	1.3	235	4	AA114545	Aal14545 Human bre	C 370	23	1.3	267	4	AAH69561	Aah69561 Human cer
C 298	23	1.3	235	4	AAH69890	Aah69890 Human pro	C 371	23	1.3	267	5	ABV37677	Abv37677 Human pro
C 299	23	1.3	235	5	ABV07568	Abv07568 Human pro	C 372	23	1.3	267	5	ABV37753	Abv37753 Human pro
C 300	23	1.3	235	5	ADI72022	Adi72022 Human ova	C 373	23	1.3	268	4	AAH70080	Aah70080 Human cer
C 301	23	1.3	235	5	ADL37171	Adl37171 Human ova	C 374	23	1.3	268	5	ABV38724	Abv38724 Human pro
C 302	23	1.3	235	5	ADI73143	Adi73143 Human ova	C 375	23	1.3	268	5	ADI73289	Adi73289 Human ova
C 303	23	1.3	236	5	ADL38276	Adl38276 Human ova	C 376	23	1.3	268	5	ADL38420	Adl38420 Human ova
C 304	23	1.3	236	10	ABT22889	Abt22889 Breast ca	C 377	23	1.3	269	4	AA116395	Aal16395 Human bre
C 305	23	1.3	237	5	ABV07534	Abv07534 Human pro	C 378	23	1.3	269	4	AAH70096	Aah70096 Human cer
C 306	23	1.3	238	4	AA507775	Aas07775 Cervical	C 379	23	1.3	269	5	ABV08018	Abv08018 Human pro
C 307	23	1.3	238	4	AAH69502	Aah69502 Human cer	C 380	23	1.3	271	4	AA116367	Aal16367 Human bre
C 308	23	1.3	241	5	ABV07986	Abv07986 Human pro	C 381	23	1.3	271	4	AAH70009	Aah70009 Human cer
C 309	23	1.3	241	5	ABV08250	Abv08250 Human pro	C 382	23	1.3	271	5	ADL43054	Adl43054 Human ova
C 310	23	1.3	241	14	ADY98867	Ady98867 T_reesei	C 383	23	1.3	271	5	ADL37357	Adl37357 Human ova
C 311	23	1.3	244	5	ABV07846	Abv07846 Human pro	C 384	23	1.3	271	5	ADL72212	Adl72212 Human ova

C 385	23	1.3	272	5	AD172411	Adi72411 Human ova
C 386	23	1.3	272	5	ADL37774	Adi37774 Human ova
C 387	23	1.3	272	5	ADI72635	Adi72635 Human ova
C 388	23	1.3	272	5	ADL37554	Adi37554 Human ova
C 389	23	1.3	273	5	ADL37629	Adi37629 Human ova
C 390	23	1.3	273	5	ADI72490	Adi72490 Human ova
C 391	23	1.3	273	6	ABV98946	Abv98946 Human pan
C 392	23	1.3	276	4	AAS07741	Aas07741 Cervical
C 393	23	1.3	277	5	ABV37613	Abv37613 Human pro
C 394	23	1.3	277	5	ABV37936	Abv37936 Human pro
C 395	23	1.3	277	14	ADY98804	Ady98804 T_reesei
C 396	23	1.3	278	6	ABQ56327	Abq56327 Human col
C 397	23	1.3	279	5	ABV07457	Abv07457 Human pro
C 398	23	1.3	279	5	ADL38694	Adi38694 Human ova
C 399	23	1.3	279	5	ADI73564	Adi73564 Human ova
C 400	23	1.3	279	5	ADL43556	Adi43556 Human ova
C 401	23	1.3	281	5	ABV35976	Abv35976 Human pro
C 402	23	1.3	282	4	AAL16353	Aal16353 Human bre
C 403	23	1.3	282	5	ABV08060	Abv08060 Human pro
C 404	23	1.3	282	5	ADL37122	Adi37122 Human ova
C 405	23	1.3	282	5	ADL38105	Adi38105 Human ova
C 406	23	1.3	282	5	ADI71972	Adi71972 Human ova
C 407	23	1.3	282	5	ADI72969	Adi72969 Human ova
C 408	23	1.3	283	5	ADI69337	Adi69337 Human ova
C 409	23	1.3	283	5	ADL44042	Adi44042 Human ova
C 410	23	1.3	283	5	ADI75681	Adi75681 Human ova
C 411	23	1.3	284	10	ABT22890	Abt22890 Breast ca
C 412	23	1.3	284	10	ABT22751	Abt22751 Breast ca
C 413	23	1.3	285	5	ABV37274	Abv37274 Human pro
C 414	23	1.3	285	12	ADQ18335	Adq18335 Human sof
C 415	23	1.3	285	14	ADY99470	Ady99470 T_reesei
C 416	23	1.3	287	5	ADI73568	Adi73568 Human ova
C 417	23	1.3	287	5	ADL38698	Adi38698 Human ova
C 418	23	1.3	287	5	ADI72856	Adi72856 Human ova
C 419	23	1.3	287	5	ADL37995	Adi37995 Human ova
C 420	23	1.3	287	14	ADY98677	Ady98677 T_reesei
C 421	23	1.3	288	4	AAS07707	Aas07707 Cervical
C 422	23	1.3	288	4	AAH69821	Aah69821 Human cer
C 423	23	1.3	288	5	ADL43929	Adi43929 Human ova
C 424	23	1.3	289	4	AAH69822	Aah69822 Human cer
C 425	23	1.3	289	5	ADL43359	Adi43359 Human ova
C 426	23	1.3	289	5	ADI71439	Adi71439 Human ova
C 427	23	1.3	289	5	ADL36597	Adi36597 Human ova
C 428	23	1.3	289	14	ADY98877	Ady98877 T_reesei
C 429	23	1.3	290	5	ABV06729	Abv06729 Human pro
C 430	23	1.3	291	5	ABV37873	Abv37873 Human pro
C 431	23	1.3	292	5	ABV07826	Abv07826 Human pro
C 432	23	1.3	293	5	ADI72045	Adi72045 Human ova
C 433	23	1.3	293	5	ADL37194	Adi37194 Human ova
C 434	23	1.3	295	4	AAS07819	Aas07819 Cervical
C 435	23	1.3	295	5	ADL38064	Adi38064 Human ova
C 436	23	1.3	295	5	ADI72927	Adi72927 Human ova
C 437	23	1.3	295	10	ABT22721	Abt22721 Breast ca
C 438	23	1.3	296	4	AAL16259	Aal16259 Human bre
C 439	23	1.3	296	5	ADL36888	Adi36888 Human ova
C 440	23	1.3	296	5	ADL38330	Adi38330 Human ova
C 441	23	1.3	296	5	ADI71733	Adi71733 Human ova
C 442	23	1.3	296	5	ADI73198	Adi73198 Human ova
C 443	23	1.3	297	4	AAL13342	Aal13342 Human bre
C 444	23	1.3	297	5	ABV06657	Abv06657 Human pro
C 445	23	1.3	297	5	ADL44514	Adi44514 Human ova
C 446	23	1.3	298	5	ABV38049	Abv38049 Human pro
C 447	23	1.3	298	5	ADI70275	Adi70275 Human ova
C 448	23	1.3	298	5	ADI76603	Adi76603 Human ova
C 449	23	1.3	299	5	ABV07684	Abv07684 Human pro
C 450	23	1.3	299	5	ADL36331	Adi36331 Human ova
C 451	23	1.3	299	5	ADI76880	Adi76880 Human ova
C 452	23	1.3	299	5	ADI70559	Adi70559 Human ova
C 453	23	1.3	299	5	ADI71171	Adi71171 Human ova
C 454	23	1.3	300	4	AAH69685	Aah69685 Human cer
C 455	23	1.3	300	5	ABV07828	Abv07828 Human pro
C 456	23	1.3	300	5	ADL37800	Adi37800 Human ova
C 457	23	1.3	300	5	ADL72661	Adi72661 Human ova
C 458	23	1.3	300	5	ADL38856	Adi38856 Human ova
C 459	23	1.3	301	5	ADI70712	Adi70712 Human ova
C 460	23	1.3	302	5	ABV07754	Abv07754 Human pro
C 461	23	1.3	303	4	AAH69954	Aah69954 Human cer
C 462	23	1.3	303	5	AAF98646	Aaf98646 Human ova
C 463	23	1.3	303	5	ADI71528	Adi71528 Human ova
C 464	23	1.3	303	5	ADL36684	Adi36684 Human ova
C 465	23	1.3	303	13	ACF84697	Acf84697 Human SIR
C 466	23	1.3	304	4	AAL16023	Aal16023 Human bre
C 467	23	1.3	304	4	AAH69642	Aah69642 Human cer
C 468	23	1.3	304	5	ABV07365	Abv07365 Human pro
C 469	23	1.3	304	5	ABV37526	Abv37526 Human pro
C 470	23	1.3	304	5	ADL37322	Adi37322 Human ova
C 471	23	1.3	304	5	ADI72176	Adi72176 Human ova
C 472	23	1.3	305	4	AAH69979	Aah69979 Human cer
C 473	23	1.3	305	5	ADL36666	Adi36666 Human ova
C 474	23	1.3	305	5	ADI71510	Adi71510 Human ova
C 475	23	1.3	306	5	ABAI1166	Abai1166 Human ner
C 476	23	1.3	306	5	ABV37665	Abv37665 Human pro
C 477	23	1.3	307	4	AAH69658	Aah69658 Human cer
C 478	23	1.3	308	4	AAS07748	Aas07748 Cervical
C 479	23	1.3	308	5	ADL36154	Adi36154 Human ova
C 480	23	1.3	308	5	ADI70991	Adi70991 Human ova
C 481	23	1.3	309	5	ADL37681	Adi37681 Human ova
C 482	23	1.3	309	5	ADI76735	Adi76735 Human ova
C 483	23	1.3	309	5	ADI72859	Adi72859 Human ova
C 484	23	1.3	309	5	ADL37998	Adi37998 Human ova
C 485	23	1.3	309	5	ADI70410	Adi70410 Human ova
C 486	23	1.3	309	5	ADL43267	Adi43267 Human ova
C 487	23	1.3	309	5	ADI72542	Adi72542 Human ova
C 488	23	1.3	310	4	AAS07753	Aas07753 Cervical
C 489	23	1.3	310	5	AAF98609	Aaf98609 Human ova
C 490	23	1.3	311	14	ADY98689	Ady98689 T_reesei
C 491	23	1.3	312	4	AAL14602	Aal14602 Human bre
C 492	23	1.3	312	4	AAH69906	Aah69906 Human cer
C 493	23	1.3	313	5	ADL44508	Adi44508 Human ova
C 494	23	1.3	313	5	ADL38460	Adi38460 Human ova
C 495	23	1.3	313	5	ADI73329	Adi73329 Human ova
C 496	23	1.3	314	5	ABV05899	Abv05899 Human pro
C 497	23	1.3	314	5	ADL38439	Adi38439 Human ova
C 498	23	1.3	314	5	ADL43941	Adi43941 Human ova
C 499	23	1.3	314	5	ADI73308	Adi73308 Human ova
C 500	23	1.3	314	10	ABT22928	Abt22928 Breast ca

ALIGNMENTS

RESULT 1

ABTL3390

ID ABTL3390 standard; DNA; 1713 BP.

XX

AC ABTL3390;

XX

DT 30-JAN-2003 (first entry)

XX

DE Breast specific related polynucleotide SEQ ID No 105.

XX

KW Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer;

KW metastatic; breast cancer; breast specific; human; ds.

XX

OS Homo sapiens.

XX

FN WO200277232-A2.

XX

PD 03-OCT-2002.

XX

PF 21-NOV-2001; 2001WO-US043815.

XX

PR 22-NOV-2000; 2000US-0252509P.

XX

PA (DIAD-) DIADEXUS INC.

XX

PI Salceda S, Macina RA, Recipon H, Pluta J, Sun Y, Liu C;
XX WPI; 2003-018927/01.
XX
XX
PT New isolated nucleic acid molecule, useful for treating breast cancer,
PT and diagnosing or monitoring the presence of metastases of breast cancer
PT in a patient.
XX
XX
PS Claim 1; Page 250-251; 377pp; English.
XX
XX The invention relates to a novel isolated nucleic acid molecule
CC comprising: a sequence encoding a sequence comprising 11-1518 amino acids
CC ; a sequence comprising 190-8144 bp; or a sequence that selectively
CC hybridizes to, or having at least 60% identity with the 11-1518 amino
CC acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are
CC useful for treating breast cancer, and diagnosing or monitoring the
CC presence of metastases of breast cancer in a patient. The polynucleotides
CC of the invention can be used to treat disorders by gene therapy. This
CC polynucleotide represents a breast specific related sequence of the
CC invention
XX
SQ Sequence 1713 BP; 344 A; 553 C; 468 G; 348 T; 0 U; 0 Other;
Query Match 100.0%; Score 1713; DB 8; Length 1713;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCCCCGCTGGACACCCCGCCAGCATCTGGGCTTCCACGCTTGGGACCGTGGGAG 60
DB 1 ATGCCCCCGCTGGACACCCCGCCAGCATCTGGGCTTCCACGCTTGGGACCGTGGGAG 60
QY 61 CGGCGAAACAGAGCTATGTCTGGAGACATATGATAAACCACTTCAGCCGCCACCAAGCCGC 120
DB 61 CGGCGAAACAGAGCTATGTCTGGAGACATATGATAAACCACTTCAGCCGCCACCAAGCCGC 120
QY 121 CGCACCCCTAGACAGACCCCAAGACCTTGGCCACCATGGCCAGAGAGCATTTACCTTC 180
DB 121 CGCACCCCTAGACAGACCCCAAGACCTTGGCCACCATGGCCAGAGAGCATTTACCTTC 180
QY 181 ATCTCTGCTCTGCTAGCCGGCCCTTGAGTTCGCCACCTGCTGCTCTCTGGCGACCC 240
DB 181 ATCTCTGCTCTGCTAGCCGGCCCTTGAGTTCGCCACCTGCTGCTCTCTGGCGACCC 240
QY 241 TGGGTGCGGAGTGTGTCGGGCTGCTTCTGCTTCCGCGCTGCGCGGATTCGCTCCAG 300
DB 241 TGGGTGCGGAGTGTGTCGGGCTGCTTCTGCTTCCGCGCTGCGCGGATTCGCTCCAG 300
QY 301 CGCTGTGAGCTGTGTCGGGGATGACAGCCCTGCTCTACTGAGGACTCCACTGAG 360
DB 301 CGCTGTGAGCTGTGTCGGGGATGACAGCCCTGCTCTACTGAGGACTCCACTGAG 360
QY 361 GGGACTGCTGAAGCCAACTGGGCCAAGAGACACATGAGTGGCCCGCCAGCCCTGATCGT 420
DB 361 GGGACTGCTGAAGCCAACTGGGCCAAGAGACACATGAGTGGCCCGCCAGCCCTGATCGT 420
QY 421 GCACCCCGCCAGCCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGAGAGCTTCAGC 480
DB 421 GCACCCCGCCAGCCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGAGAGCTTCAGC 480
QY 481 TACCCCGATGTTAAGCTCAAGGCAATCCCTGTGTATCCCTACCCAGAGGCGACCTCCCA 540
DB 481 TACCCCGATGTTAAGCTCAAGGCAATCCCTGTGTATCCCTACCCAGAGGCGACCTCCCA 540
QY 541 GCCCTGATGGGACTCTGCTGCAAGGAGCCACTGGCCGATCCGCCACCATGCGACAC 600
DB 541 GCCCTGATGGGACTCTGCTGCAAGGAGCCACTGGCCGATCCGCCACCATGCGACAC 600
QY 601 AGCTGCCAGCACCTTTGCCAGTAGTCTCTGCTGCTCCGAGGAGTACTATTCTTTCCAT 660
DB 601 AGCTGCCAGCACCTTTGCCAGTAGTCTCTGCTGCTCCGAGGAGTACTATTCTTTCCAT 660
QY 661 GAGTCGAGACCTTCGCGAGATGGCGAGTGGCTCCATGTCGAGCCGAGAAATTGAT 720
DB 661 GAGTCGAGACCTTCGCGAGATGGCGAGTGGCTCCATGTCGAGCCGAGAAATTGAT 720

DB 661 GAGTCGAGACCTTCGCGAGATGGCGAGTGGCTCCATGTCGAGCCGAGAAATTGAT 720
QY 721 GTGCTCATCTTTCAAGAAAGCTGACAGAGCTGTTACGCGTACACCAAGATCGATGAGCTGGCC 780
DB 721 GTGCTCATCTTTCAAGAAAGCTGACAGAGCTGTTACGCGTACACCAAGATCGATGAGCTGGCC 780
QY 781 AAGTGCACATCAGACACTGTGTTCTTCTGGAGAGACCAAGTAAAGTCTCGGACCTTATCAGC 840
DB 781 AAGTGCACATCAGACACTGTGTTCTTCTGGAGAGACCAAGTAAAGTCTCGGACCTTATCAGC 840
QY 841 AGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGGCGCGCTGTGTACGCGGC 900
DB 841 AGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGGCGCGCTGTGTACGCGGC 900
QY 901 ATCAATTGCAATTAGTACCCGAAAGAGCGTCTCGCCACACAGACTCTCGAGGGTCTGTCA 960
DB 901 ATCAATTGCAATTAGTACCCGAAAGAGCGTCTCGCCACACAGACTCTCGAGGGTCTGTCA 960
QY 961 ACTCGGGTGTGTCGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGCTGGGC 1020
DB 961 ACTCGGGTGTGTCGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGCTGGGC 1020
QY 1021 TCAGGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGACGACTGCAGATGCC 1080
DB 1021 TCAGGTCTCAGCCAGGATGAGTGCAGTGCAGATCTCCAGGAGACGACTGCAGATGCC 1080
QY 1081 ATCCGCCGAAAGCTGAGGCTTATGGAGCTCCAGGGTACCCAGCAAGCATGACTCATCC 1140
DB 1081 ATCCGCCGAAAGCTGAGGCTTATGGAGCTCCAGGGTACCCAGCAAGCATGACTCATCC 1140
QY 1141 TTCAGGACACCGACACAGACTCGTTCGGGGGACACCTTGTCTCCAGGTGTACTGTAAACC 1200
DB 1141 TTCAGGACACCGACACAGACTCGTTCGGGGGACACCTTGTCTCCAGGTGTACTGTAAACC 1200
QY 1201 CTGCGAGCCGAGCTGCCACACCTTTCTGGGAGAGCATGGCTTACAGAAATGAAGAGGG 1260
DB 1201 CTGCGAGCCGAGCTGCCACACCTTTCTGGGAGAGCATGGCTTACAGAAATGAAGAGGG 1260
QY 1261 GGACAGGAAACCCCTGTGGGAGAGCTTGAACCTGGAAGAGTGGCCACTTGGCTCTCC 1320
DB 1261 GGACAGGAAACCCCTGTGGGAGAGCTTGAACCTGGAAGAGTGGCCACTTGGCTCTCC 1320
QY 1321 TGCCTTGGCTGACTGGGTTCTTGACACCATGTCATTTTCACTGGGCCATGGGATCTACATC 1380
DB 1321 TGCCTTGGCTGACTGGGTTCTTGACACCATGTCATTTTCACTGGGCCATGGGATCTACATC 1380
QY 1381 TCCTTGGCATCCCGAGCTGGTCTGATCCCTGCGAGGGCCCTTCTCTCTGCTCATGGTCT 1440
DB 1381 TCCTTGGCATCCCGAGCTGGTCTGATCCCTGCGAGGGCCCTTCTCTCTGCTCATGGTCT 1440
QY 1441 TCAGGTGGCTGTGATCATGGAAGTAAAGGAGTTAGGCAATTACCTCTGGGAGTGAACCCCTG 1500
DB 1441 TCAGGTGGCTGTGATCATGGAAGTAAAGGAGTTAGGCAATTACCTCTGGGAGTGAACCCCTG 1500
QY 1501 ACTCATCCCTTATTTGCCACCTTAAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAAT 1560
DB 1501 ACTCATCCCTTATTTGCCACCTTAAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAAT 1560
QY 1561 TCAACAGTTAAAGAGCTTATCTTAAATGTTATTTGGGGGTGGGAGGGCCCACT 1620
DB 1561 TCAACAGTTAAAGAGCTTATCTTAAATGTTATTTGGGGGTGGGAGGGCCCACT 1620
QY 1621 CTATGTTATGTTAAGGAGTGGTCTGTTCTGTTCTTGGCTGATGTTCTGTTATCTTAAATGAC 1680
DB 1621 CTATGTTATGTTAAGGAGTGGTCTGTTCTGTTCTTGGCTGATGTTCTGTTATCTTAAATGAC 1680
QY 1681 CACAGTTGTTAAGTACCTTCGCGCGGACCAAGC 1713
DB 1681 CACAGTTGTTAAGTACCTTCGCGCGGACCAAGC 1713

AD001260 standard; cDNA; 2392 BP.	Matches 1695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
ADD01260;	
01-JAN-2004 (first entry)	
Human nucleic acid-associated protein NAAP-41 cDNA SEQ ID NO:98.	
human; nucleic acid-associated protein; NAAP; cytosolic;	
antiarteriosclerotic; anti-HIV; anti-allergic; cerebroprotective;	
antiparkinsonian; anticonvulsant; neurotropic; neuroprotective;	
antiinflammatory; ophthalmological; thyromimetic; antiarthritic;	
hepatotropic; antibacterial; virucide; protozoacide; antiparasitic;	
fungicide; gene therapy; cell proliferative disease; cancer;	
atherosclerosis; hepatitis; neurological disorder; Parkinson's disease;	
Alzheimer's disease; stroke; epilepsy; developmental disorder;	
renal tubular acidosis; anaemia; glaucoma; hypothyroidism;	
autoimmune disorder; inflammatory disorder; AIDS; allergy;	
atopic dermatitis; arthritis; infection; gene; ss.	
Homo sapiens.	
WO2003054219-A2.	
03-JUL-2003.	
18-DEC-2002; 2002WO-US041115.	
19-DEC-2001; 2001US-0343004P.	
11-JAN-2002; 2002US-0347633P.	
25-JAN-2002; 2002US-0351749P.	
22-FEB-2002; 2002US-0359498P.	
(INCY-) INCYTE GENOMICS INC.	
Azimzai Y, Baughn MR, Becha SD, Borowsky ML, Burford N;	
Elliot V8, Emerling BM, Forsythe IJ, Gorvad AE, Griffin JA;	
Kable AE, Khare R, Lal PG, Lee EA, Lee SY, Li JX, Marquis JP;	
Rankumar J, Richardson TW, Sprague WW, Swarnakar A, Tang YT;	
Chawla NK, Warren BA, Yue H;	
WPI; 2003-559157/52.	
P-PSDB; ADD01203.	
New human nucleic acid-associated proteins (NAAP), useful for diagnosing,	
treating and preventing diseases or conditions associated with the	
aberrant NAAP expression, e.g. cancer, hepatitis, AIDS, atherosclerosis,	
infections.	
Claim 5; SEQ ID NO 98; 405pp; English.	
The present invention describes human nucleic acid-associated proteins	
designated NAAP-1 to NAAP-57. The human NAAPs have cytosolic,	
antiarteriosclerotic, anti-HIV, anti-allergic, cerebroprotective,	
antiparkinsonian, anticonvulsant, neurotropic, neuroprotective,	
antiinflammatory, ophthalmological, thyromimetic, antiarthritic,	
hepatotropic, antibacterial, virucide, protozoacide, antiparasitic and	
fungicide activities, and can be used in gene therapy. The NAAP protein	
and polynucleotide sequences can be used in diagnosing, treating and	
preventing diseases or conditions associated with the decreased	
expression or overexpression of NAAP, such as cell proliferative diseases	
(e.g. cancer, atherosclerosis, hepatitis), neurological disorders	
(Parkinson's disease, Alzheimer's disease, stroke, epilepsy),	
developmental disorders (renal tubular acidosis, anaemia, glaucoma,	
hypothyroidism), autoimmune/inflammatory disorders (AIDS, allergies,	
atopic dermatitis, arthritis) and infections (e.g. bacterial, viral,	
parasitic, protozoal, fungal). The present sequence encodes human NAAP-	
41, from the present invention.	
Sequence 2392 BP; 471 A; 743 C; 674 G; 504 T; 0 U; 0 Other;	
Query Match 96.0%; Score 1645; DB 10; Length 2392;	
Best Local Similarity 99.9%; Pred. No. 0;	


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Qy 361 GGGAGTCTGAAGCCAACTGGGCCAAGGAGCACAAATGGAGTGGCCCCCAGACCCCTGATCGT 420
Db 450 GGGAGTCTGAAGCCAACTGGGCCAAGGAGCACAAATGGAGTGGCCCCCAGACCCCTGATCGT 509
Qy 421 GCACCCCCCAGCCGCGGGATGGCCAGCGGGCTCAAGTCAACCATGGGCGAGAGCTTCAGC 480
Db 510 GCACCCCCCAGCCGCGGGATGGCCAGCGCTCAAGTCAACCATGGGCGAGAGCTTCAGC 569
Qy 481 TACCCCGATGTAAAGCTCAAAAGGCAATCCCTGTGTATCCCTACCCAGAGGCCACCTCCCCA 540
Db 570 TACCCCGATGTAAAGCTCAAAAGGCAATCCCTGTGTATCCCTACCCAGAGGCCACCTCCCCA 629
Qy 541 GCCCTGATGCGGACTCTCTGCTGCAAGGAGCACTGGCCGATCCCCACCCATCGGACAC 600
Db 630 GCCCTGATGCGGACTCTCTGCTGCAAGGAGCACTGGCCGATCCCCACCCATCGGACAC 689
Qy 601 AGCTTGCCCGACACCTTTGCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTCTTTTCCAT 660
Db 690 AGCTTGCCCGACACCTTTGCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTCTTTCCAT 749
Qy 661 GAGTCGACCTGAGACTCTCCGAGAGATGGGCGAGTGGCTCCATGTGAGCCGAGAAATGTAT 720
Db 750 GAGTCGACCTGAGACTCTCCGAGAGATGGGCGAGTGGCTCCATGTGAGCCGAGAAATGTAT 809
Qy 721 GTGCTCATCTTCAAGAGCTCACAGAGCTGTTCAAGCGTACACAGATCGATGAGCTGGCC 780
Db 810 GTGCTCATCTTCAAGAGCTCACAGAGCTGTTCAAGCGTACACAGATCGATGAGCTGGCC 869
Qy 781 AAGTGCAATCAGACACTGTGTTCTCGAGAGACCCAGTAAAGATCTCGACCTTTATCAGC 840
Db 870 AAGTGCAATCAGACACTGTGTTCTCGAGAGACCCAGTAAAGATCTCGACCTTTATCAGC 929
Qy 841 AGCATACGAGAGACTACCACTGATGAGCAGAGATGCTGAGGGCGGCTGGTACGGGC 900
Db 930 AGCATACGAGAGACTACCACTGATGAGCAGAGATGCTGAGGGCGGCTGGTACGGGC 989
Qy 901 ATCATTCGCATTAGTACCGAAAGCGTCTCGCCACAGACTCGGAGGGTCGTTCAC 960
Db 990 ATCATTCGCATTAGTACCGAAAGCGTCTCGCCACAGACTCGGAGGGTCGTTCAC 1049
Qy 961 ACTCGGGTGTGTCGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGCTGGGC 1020
Db 1050 ACTCGGGTGTGTCGCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGCTGGGC 1109
Qy 1021 TCAGGTCTACCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC 1080
Db 1110 TCAGGTCTACCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGATGCC 1169
Qy 1081 ATCGCCGGAAGCTGAGSCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 1140
Db 1170 ATCGCCGGAAGCTGAGSCCTTATGGAGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 1229
Qy 1141 TTCCAGGSCACCGACACAGACTCGTTCGGGGGCACCCCTTGCTTCCAGGTGTACTGCTAACCC 1200
Db 1230 TTCCAGGSCACCGACACAGACTCGTTCGGGGGCACCCCTTGCTTCCAGGTGTACTGCTAACCC 1289
Qy 1201 CTGCCAGGCCAGCTGCGCACACCTTTCTGGGAGAGCATGGCTTACAGAATGAAGAGGG 1260
Db 1290 CTGCCAGGCCAGCTGCGCACACCTTTCTGGGAGAGCATGGCTTACAGAATGAAGAGGG 1349
Qy 1261 GGACCCAGAACCTCTGTGGGAGGCTTAGACCTGMAAGCAGTGGCCCACTCTGGCTCTCTCC 1320
Db 1350 GGACCCAGAACCTCTGTGGGAGGCTTAGACCTGMAAGCAGTGGCCCACTCTGGCTCTCTCC 1409
Qy 1321 TGCCTTGCTGACTGGGTCTCTGGACCATGTGCAATTTTCACTGGGCCATGGGATCTACATC 1380
Db 1410 TGCCTTGCTGACTGGGTCTCTGGACCATGTGCAATTTTCACTGGGCCATGGGATCTACATC 1469
Qy 1381 TCCTTGCAATCCCGAGCTGGTCTGATCCCTGCGAGGGCCCTTCTCTCTGCTCATGTCT 1440
Db 1470 TCCTTGCAATCCCGAGCTGGTCTGATCCCTGCGAGGGCCCTTCTCTCTGCTCATGTCT 1529
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Qy 1441 TCAGTGGCCCTGATCATGGAAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAACCCCTG 1500
Db 1530 TCAGTGGCCCTGATCATGGAAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAACCCCTG 1589
Qy 1501 ACTCCATCCCCCTATTGCCACCCCTAAACCAATCATGCAAACTTCTCCCTCTGGGGTAAT 1560
Db 1590 ACTCCATCCCCCTATTGCCACCCCTAAACCAATCATGCAAACTTCTCCCTCTGGGGTAAT 1649
Qy 1561 TCACAGTTAAAGAGCTTATCTTAATGTATTGTATTGGGGGTGGGCGAGGCCCACT 1620
Db 1650 TCACAGTTAAAGAGCTTATCTTAATGTATTGTATTGGGGGTGGGCGAGGCCCACT 1709
Qy 1621 CTATGTTATGTTAAGGAGTTGGTTCTGCTTCTGGCTGATGTTCTGTATCTTAACATGAC 1680
Db 1710 CTATGTTATGTTAAGGAGTTGGTTCTGCTTCTGGCTGATGTTCTGTATCTTAACATGAC 1769
Qy 1681 CACAGTTTGTAAAGTAC 1696
Db 1770 CACAGTTTGTAAAGTAC 1785

RESULT 4
ABX92075
ID ABX92075 standard; cDNA; 1977 BP.
XX
AC ABX92075;
XX
DT 08-MAY-2003 (first entry)
XX
DE Lung specific nucleic acid (LSNA) #117.
XX
KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200268633-A2.
XX
PD 06-SEP-2002.
XX
PF 21-NOV-2001; 2001WO-US043612.
XX
PR 22-NOV-2000; 2000US-0252500P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX
PS WPI; 2002-713376/77.
XX
PT New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.
XX
PS Claim 1; Page 266-267; 389pp; English.
XX
CC The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the
CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This sequence
CC encodes a lung specific nucleic acid
XX
SQ Sequence 1977 BP; 393 A; 631 C; 554 G; 399 T; 0 U; 0 Other;
Query Match 57.4%; Score 983; DB 6; Length 1977;
Best Local Similarity 99.9%; Pred. No. 0;
```

Matches 1103; Conservative 0; Mismatches 0; Indels 1; Gaps 1;			
Qy	598	CACAGCTGCCAGACCTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTC	657
Db	861	CACAGCTGCCAGACCTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTC	920
Qy	658	CATGAGTCGGACCTGGACCTGCCGAGATGGCAGTGGCTCATGTCCAGCCGAGAAATT	717
Db	921	CATGAGTCGGACCTGGACCTGCCGAGATGGCAGTGGCTCATGTCCAGCCGAGAAATT	980
Qy	718	GATGTGCTCATCTTCAAGAAGCTGACAGA-GCTGTTCAGCGGTACACACAGATCGATGAGCT	776
Db	981	GATGTGCTCATCTTCAAGAAGCTGACAGA-GCTGTTCAGCGGTACACACAGATCGATGAGCT	1040
Qy	777	GGCCAAAGTGCACATCAGACACTGTGTTCTTGAGAAAGACCAAGTAAAGTCTCGACCTTAT	836
Db	1041	GGCCAAAGTGCACATCAGACACTGTGTTCTTGAGAAAGACCAAGTAAAGTCTCGACCTTAT	1100
Qy	837	CAGCAGCATCAGCAGGACTACCACTCGATGAGCAGGATGCTGAGGCGCCGCTGGTACG	896
Db	1101	CAGCAGCATCAGCAGGACTACCACTCGATGAGCAGGATGCTGAGGCGCCGCTGGTACG	1160
Qy	897	CGGCATCATTCGATTTAGTACCCGAAAGACCGTCTGCCACACAGACTCGGAGGGTCG	956
Db	1161	CGGCATCATTCGATTTAGTACCCGAAAGACCGTCTGCCACACAGACTCGGAGGGTCG	1220
Qy	957	TTCAACTCGGGTGTGTCGCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGT	1016
Db	1221	TTCAACTCGGGTGTGTCGCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGT	1280
Qy	1017	GGGCTCAGGTTCCAGCAGATGAGTGCAGTGCAGATCTCCGAGGAGACGCTGCAGA	1076
Db	1281	GGGCTCAGGTTCCAGCAGATGAGTGCAGTGCAGATCTCCGAGGAGACGCTGCAGA	1340
Qy	1077	TGCCATGCCCGGAGCTGAGSCCTTATGGAGTCCAGGCTACCCAGCAAGCCATGACTC	1136
Db	1341	TGCCATGCCCGGAGCTGAGSCCTTATGGAGTCCAGGCTACCCAGCAAGCCATGACTC	1400
Qy	1137	ATCCTTCCAGGGCACCGACACAGACTCGTGGGGGACCCCTTGTCTCCAGGTGTACTGCTA	1196
Db	1401	ATCCTTCCAGGGCACCGACACAGACTCGTGGGGGACCCCTTGTCTCCAGGTGTACTGCTA	1460
Qy	1197	ACCCCTGCCAGGCCAGCTGCCACACCTTTCTGGGAGAGATGGCCCTACAGATGAAG	1256
Db	1461	ACCCCTGCCAGGCCAGCTGCCACACCTTTCTGGGAGAGATGGCCCTACAGATGAAG	1520
Qy	1257	AGGGGACCGAAGCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCCTCTGGCTC	1316
Db	1521	AGGGGACCGAAGCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCCTCTGGCTC	1580
Qy	1317	CTCCTGCTTGGCTGACTGGGTTCTTGACCATGTGCAATTTCACTGGGCCATGGGATCTA	1376
Db	1581	CTCCTGCTTGGCTGACTGGGTTCTTGACCATGTGCAATTTCACTGGGCCATGGGATCTA	1640
Qy	1377	CATCTCTTGATCCCAAGCTGGTCTGATCCCTGTCAGGGCCCTTCTCTGCTCATG	1436
Db	1641	CATCTCTTGATCCCAAGCTGGTCTGATCCCTGTCAGGGCCCTTCTCTGCTCATG	1700
Qy	1437	GTCTTCAGTGGCCTGATCATGGAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAAC	1496
Db	1701	GTCTTCAGTGGCCTGATCATGGAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAAC	1760
Qy	1497	CCTGACTCCATCCCTTATTCGCCACCTTAAACCAATCATGCCTTCTCCCTCCCTGGGG	1556
Db	1761	CCTGACTCCATCCCTTATTCGCCACCTTAAACCAATCATGCCTTCTCCCTCCCTGGGG	1820
Qy	1557	TAAATCAACAGTTAAAGAAGCTTATCTTAAATGATTTGATTTGGGGGGTGGCGAGGCC	1616
Db	1821	TAAATCAACAGTTAAAGAAGCTTATCTTAAATGATTTGATTTGGGGGGTGGCGAGGCC	1880
Qy	1617	CACCTATGTTATGTTAAGGAGTTGGTTCCTGGTCTTGGCTGATGTTCTGTATCTTAACA	1676
Db	1891	CACCTATGTTATGTTAAGGAGTTGGTTCCTGGTCTTGGCTGATGTTCTGTATCTTAACA	1940

Qy	1677	TGACCACAGTTTGTAAAGTACCTCG	1700
Db	1941	TGACCACAGTTTGTAAAGTACCTCG	1964
RESULT 5			
ID	ABX92014	standard; cDNA; 1977 BP.	
AC	ABX92014;		
DT	08-MAY-2003	(first entry)	
XX	Lung specific nucleic acid (LSNA) #56.		
DE	Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;		
KW	cancer monitoring; cancer staging; cancer imaging; lung cancer;		
KW	non-cancerous diseases of the lung; transgenic animal; gene; ss.		
OS	Homo sapiens.		
XX	WO200268633-A2.		
PN	06-SEP-2002.		
PD	21-NOV-2001; 2001WO-US043612.		
PF	22-NOV-2000; 2000US-0252500P.		
PR	(DIAD-) DIADEXUS INC.		
XX	Macina RA, Recipon H, Chen S, Sun Y, Liu C;		
PI	WPI; 2002-713376/77.		
DR	New isolated human nucleic acid molecule and polypeptide, useful for		
XX	identifying, diagnosing, monitoring, staging, imaging and treating lung		
PT	cancer and non-cancerous diseases of the lung.		
PT	Claim 1; Page 205-206; 389pp; English.		
XX	The invention describes an isolated human nucleic acid (I) encoding any		
CC	of 120 10-1533 residue amino acid sequences (S1), given in the		
CC	specification, comprising any of 164 179-12421 base pair sequences (S2),		
CC	given in the specification. The methods and compositions of the present		
CC	invention are useful for identifying, diagnosing, monitoring, staging,		
CC	imaging and treating lung cancer and non-cancerous diseases of the lung.		
CC	They are also used for identifying lung tissue, monitoring and		
CC	identifying and/or designing antagonists of the polypeptide of the		
CC	invention, gene therapy, production of transgenic animals and production		
CC	of engineered lung tissue for treatment and research. This sequence		
CC	encodes a lung specific nucleic acid		
XX	Sequence 1977 BP; 393 A; 631 C; 554 G; 399 T; 0 U; 0 Other;		
SQ	Query Match 57.4%; Score 983; DB 6; Length 1977;		
	Best Local Similarity 99.9%; Pred. No. 0;		
	Matches 1103; Conservative 0; Mismatches 0; Indels 1; Gaps 1;		
Qy	598	CACAGCTGCCAGACCTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTC	657
Db	861	CACAGCTGCCAGACCTTTGCCAGTAGTCTCTGTGGCTCCGAGGAGTACTATTCTTTC	920
Qy	658	CATGAGTCGGACCTGGACCTGCCGAGATGGCAGTGGCTCATGTCCAGCCGAGAAATT	717
Db	921	CATGAGTCGGACCTGGACCTGCCGAGATGGCAGTGGCTCATGTCCAGCCGAGAAATT	980
Qy	718	GATGTGCTCATCTTCAAGAAGCTGACAGA-GCTGTTCAGCGGTACACACAGATCGATGAGCT	776
Db	981	GATGTGCTCATCTTCAAGAAGCTGACAGA-GCTGTTCAGCGGTACACACAGATCGATGAGCT	1040
Qy	777	GGCCAAAGTGCACATCAGACACTGTGTTCTTGAGAAAGACCAAGTAAAGTCTCGGACCTTAT	836

Db 1041 GCCAAGTGCATCAGACACTGTGTTCTCGAGAGACCAAGTAAAGTCTCGGACCTTAT 1100
Qy 837 CAGCAGCATCAGCAGGACTACCACTGGATGAGCAGATGCTGAGGCCCTCGGTACG 896
Db 1101 CAGCAGCATCAGCAGGACTACCACTGGATGAGCAGATGCTGAGGCCCTCGGTACG 1160
Qy 897 CGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCACACAGACTCGGAGGGTCG 956
Db 1161 CGGCATCATTCGCATTAGTACCCGAAAGAGCCGTGCTCGCCACACAGACTCGGAGGGTCG 1220
Qy 957 TTCAACTCGGCTGCTGCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGT 1016
Db 1221 TTCAACTCGGCTGCTGCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGGT 1280
Qy 1017 GGGCTCAGGCTCAGCCAGATGAGCTGACAGTGCAGATCTCCAGGAGCAGCTGCAGA 1076
Db 1281 GGGCTCAGGCTCAGCCAGATGAGCTGACAGTGCAGATCTCCAGGAGCAGCTGCAGA 1340
Qy 1077 TGCCATCGCCCGAAGCTGAGGCCCTTATGGAGCTCCAGGGTACCAGCAAGCCATGACTC 1136
Db 1341 TGCCATCGCCCGAAGCTGAGGCCCTTATGGAGCTCCAGGGTACCAGCAAGCCATGACTC 1400
Qy 1137 ATCCTTCCAGGGCACCGACACAGACTCGTCGGGGGACCCCTTGCTCCAGGTGTACTGCTA 1196
Db 1401 ATCCTTCCAGGGCACCGACACAGACTCGTCGGGGGACCCCTTGCTCCAGGTGTACTGCTA 1460
Qy 1197 ACCCTGCGAGCCAGCTGACACACACCTTCTCGGAGAGCATGGCTCAGCAATGAAG 1256
Db 1461 ACCCTGCGAGCCAGCTGACACACACCTTCTCGGAGAGCATGGCTCAGCAATGAAG 1520
Qy 1257 AGGGGACCGAAGACCCCTGTGGAGAGGCTTAGACCTGAAGAGTGCCCACTCTGGCTC 1316
Db 1521 AGGGGACCGAAGACCCCTGTGGAGAGGCTTAGACCTGAAGAGTGCCCACTCTGGCTC 1580
Qy 1317 CTCCTGCTTGGCTGACTGGGTTCTCGGACCATGTGCATTTTCACTGGGCGCATGGGATCTA 1376
Db 1581 CTCCTGCTTGGCTGACTGGGTTCTCGGACCATGTGCATTTTCACTGGGCGCATGGGATCTA 1640
Qy 1377 CATCTCTTGATCCCGAGCTGGTCTGATCCCTGCGAGGGCCCTTCTCTCTGCTCATG 1436
Db 1641 CATCTCTTGATCCCGAGCTGGTCTGATCCCTGCGAGGGCCCTTCTCTCTGCTCATG 1700
Qy 1437 GTCTTCAGTGGCTGATCATGGAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAAC 1496
Db 1701 GTCTTCAGTGGCTGATCATGGAAGTAAGGAGTTAGGCATTACCTTCTGGGAGTGAAC 1760
Qy 1497 CCTGACTCCATPCCCTTATTCGCCACCCCTAACCAATCATGCAAACTTCTCCCTCGGG 1556
Db 1761 CCTGACTCCATPCCCTTATTCGCCACCCCTAACCAATCATGCAAACTTCTCCCTCGGG 1820
Qy 1557 TAATTCACAGTTAAAGAGCTTATCTTAATGATTTGATTTGGGGGTGGGCGAGGCC 1616
Db 1821 TAATTCACAGTTAAAGAGCTTATCTTAATGATTTGATTTGGGGGTGGGCGAGGCC 1880
Qy 1617 CACTCTATGTTATGTTAAGAGTTGGTCTCGTCTTGGCTGATGTTCTGATCTTAAACA 1676
Db 1881 CACTCTATGTTATGTTAAGAGTTGGTCTCGTCTTGGCTGATGTTCTGATCTTAAACA 1940
Qy 1677 TGACCACAGTTTGTAAAGTACCTCG 1700
Db 1941 TGACCACAGTTTGTAAAGTACCTCG 1964

RESULT 6
AEA19545
ID AEA19545 standard; cDNA; 791 BP.
XX AC AEA19545;
XX AC AEA19545;
DT 11-AUG-2005 (first entry)
XX DE Novel human polynucleotide SEQ ID NO 239.

XX vulnary; CNS-gen.; gene therapy; diagnostic; forensic; mapping;
KW DNA purification; protein purification; osteoarthritis; antiarthritic;
KW osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;
KW periodontal disease; antiinflammatory; mouth disease; burns; injury;
KW peripheral neuropathy; Alheimers disease; neuroprotective; nootropic;
KW degeneration; parkinsons disease; antiparkinsonian; neurological disease;
KW cerebrovascular ischemia; cerebroprotective; vasotropic;
KW cardiovascular disease; autoimmune disease; immunosuppressive;
KW immune disorder; viral infection; virucide; infection; cancer;
KW cytostatic; neoplasm; gene; ss.
XX Homo sapiens.
XX WO2005049806-A2.
PD 02-JUN-2005.
XX 11-MAR-2004; 2004WO-US007412.
PF 14-MAR-2003; 2003US-00389559.
XX (NUVE-) NUVELO INC.
XX Tang TY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;
PI Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;
PI Wehrman T, Weng G, Boyle B;
XX MPI; 2005-417730/42.
DR P-PSDB; AEA20112.
XX New polynucleotide encoding a polypeptide with biological activity,
PT useful for treating a disease or disorder, e.g. osteoarthritis, burns,
PT CNS and peripheral disease, stroke, autoimmune disorders, viral
PT infection, or cancer.
XX Claim 1; SEQ ID NO 239; 500pp; English.
XX The invention describes a new isolated polynucleotide (I) encoding a
CC polypeptide with biological activity comprising: a nucleotide sequence of
CC SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes
CC to the sequence of (i) under stringent hybridization conditions; or a
CC nucleotide sequence having greater than 9% sequence identity with the
CC sequence of (i). Also described are: a(n) (expression) vector comprising
CC (I); a host cell genetically engineered to comprise (I) operatively,
CC associated with a regulatory sequence that modulates expression of the
CC polynucleotide in the host cell; an isolated polypeptide comprising a
CC sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
CC is: a polypeptide encoded by (I); or a polypeptide encoded by a
CC polynucleotide hybridizing under stringent conditions with any one of SEQ
CC ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
CC carrier; an antibody directed against the polypeptide of (3); a method
CC for detecting (I) in a sample; a method for identifying a compound that binds to the
CC polypeptide of (3); a method for producing the polypeptide of (3); and a
CC collection of polynucleotides, where the collection comprising of at
CC least one of SEQ ID NOS: 1-567. (I) is a polynucleotide comprising any of
CC the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
CC activity, which comprises any of the amino acid sequence of SEQ ID NOS:
CC 568-1134. All sequences are fully defined in the specification. The
CC sequences and methods are useful in diagnostics, forensic, and gene
CC mapping, in identifying of mutations responsible for genetic disorders or
CC other traits, in assessing biodiversity, and for producing many other
CC types of data and products dependent on DNA and amino acid sequences. The
CC composition and method are useful for treating a disease or disorder,
CC e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
CC autoimmune disorders, viral infection, or cancer. This sequence encodes a
CC novel polypeptide of the invention.
XX SQ Sequence 791 BP; 149 A; 278 C; 222 G; 142 T; 0 U; 0 Other;
Query Match 39.9%; Score 683; DB 14; Length 791;

KW gene therapy; cytostatic; gene; ss.
XX Homo sapiens.
OS WO200264611-A1.
XX 22-AUG-2002.
XX 12-FEB-2002; 2002WO-US004197.
XX 13-FEB-2001; 2001US-0268292P.
XX (DIAD-) DIADEXUS INC.
XX Salceda S, Macina RA, Hu P, Recipon H, Karra K, Caferkey R;
PI Sun Y, Liu C;
FI
XX WPI; 2002-657582/70.
XX New breast specific nucleic acids and proteins, useful for identifying,
XX diagnosing, monitoring, staging, imaging, and treating breast cancer and
XX non-cancerous disease states in breast tissue, and in gene therapy.
XX Claim 1; Page 248; 367pp; English.
XX The present invention provides human breast specific coding sequences and
XX proteins. These can be used in the diagnosis and treatment of breast
XX cancer and non-cancerous diseases of the breast. The present sequence is
XX a coding sequence of the invention
SQ Sequence 386 BP; 81 A; 121 C; 94 G; 90 T; 0 U; 0 Other;

Query Match 22.1%; Score 378; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 8.2e-171;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 GCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCTACAGAAATGAAGAGGGG 1262
DB 9 GCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCTACAGAAATGAAGAGGGG 68

QY 1263 ACCAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCCTACAGAAATGAAGAGGGG 1322
DB 69 ACCAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCCTACAGAAATGAAGAGGGG 128

QY 1323 CTTGGCTGACTGGGTTCTTGGACCATGTGCATTTCACTGGGCCCATGGGATCTACATCTC 1382
DB 129 CTTGGCTGACTGGGTTCTTGGACCATGTGCATTTCACTGGGCCCATGGGATCTACATCTC 188

QY 1383 CTTGCATCCCCAGCTGGTCTGATCCCTGCCAGGCCCTTCTTCTCTGCTCATGGTCTTC 1442
DB 189 CTTGCATCCCCAGCTGGTCTGATCCCTGCCAGGCCCTTCTTCTCTGCTCATGGTCTTC 248

QY 1443 AGTGGCTGATCATGAAAGTAAGAGTTAGGCATTTACCTTCTGGAGTGAACCCCTGAC 1502
DB 249 AGTGGCTGATCATGAAAGTAAGAGTTAGGCATTTACCTTCTGGAGTGAACCCCTGAC 308

QY 1503 TCCATCCCCCTATTGGCCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAATTC 1562
DB 309 TCCATCCCCCTATTGGCCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAATTC 368

QY 1563 AACAGTTAAAGAAGCTT 1580
DB 369 AACAGTTAAAGAAGCTT 386

RESULT 9
ID ABT13389
XX ABT13389 standard; DNA; 386 BP.
XX
AC ABT13389;
XX
DT 30-JAN-2003 (first entry)
XX

DE Breast specific related polynucleotide SEQ ID No 104.
XX Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer;
KW metastatic; breast cancer; breast specific; human; ds.
XX Homo sapiens.
OS WO200277232-A2.
XX 03-OCT-2002.
XX 21-NOV-2001; 2001WO-US043815.
XX 22-NOV-2000; 2000US-0252509P.
XX (DIAD-) DIADEXUS INC.
XX Salceda S, Macina RA, Recipon H, Pluta J, Sun Y, Liu C;
PI WPI; 2003-018927/01.
XX New isolated nucleic acid molecule, useful for treating breast cancer,
PT and diagnosing or monitoring the presence of metastases of breast cancer,
PT in a patient.
XX Claim 1; Page 250; 377pp; English.
XX The invention relates to a novel isolated nucleic acid molecule
CC comprising a sequence encoding a sequence comprising 11-1518 amino acids
CC ; a sequence comprising 190-8144 bp; or a sequence that selectively
CC hybridises to, or having at least 60% identity with the 11-1518 amino
CC acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are
CC useful for treating breast cancer, and diagnosing or monitoring the
CC presence of metastases of breast cancer in a patient. The polynucleotides
CC of the invention can be used to treat disorders by gene therapy. This
CC polynucleotide represents a breast specific related sequence of the
CC invention
XX
SQ Sequence 386 BP; 81 A; 121 C; 94 G; 90 T; 0 U; 0 Other;

Query Match 22.1%; Score 378; DB 8; Length 386;
Best Local Similarity 100.0%; Pred. No. 8.2e-171;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 GCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCTACAGAAATGAAGAGGGG 1262
DB 9 GCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCTACAGAAATGAAGAGGGG 68

QY 1263 ACCAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCCTACAGAAATGAAGAGGGG 1322
DB 69 ACCAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCCTACAGAAATGAAGAGGGG 128

QY 1323 CTTGGCTGACTGGGTTCTTGGACCATGTGCATTTCACTGGGCCCATGGGATCTACATCTC 1382
DB 129 CTTGGCTGACTGGGTTCTTGGACCATGTGCATTTCACTGGGCCCATGGGATCTACATCTC 188

QY 1383 CTTGCATCCCCAGCTGGTCTGATCCCTGCCAGGCCCTTCTTCTCTGCTCATGGTCTTC 1442
DB 189 CTTGCATCCCCAGCTGGTCTGATCCCTGCCAGGCCCTTCTTCTCTGCTCATGGTCTTC 248

QY 1443 AGTGGCTGATCATGAAAGTAAGAGTTAGGCATTTACCTTCTGGAGTGAACCCCTGAC 1502
DB 249 AGTGGCTGATCATGAAAGTAAGAGTTAGGCATTTACCTTCTGGAGTGAACCCCTGAC 308

QY 1503 TCCATCCCCCTATTGGCCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAATTC 1562
DB 309 TCCATCCCCCTATTGGCCACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAATTC 368

QY 1563 AACAGTTAAAGAAGCTT 1580
DB 369 AACAGTTAAAGAAGCTT 386

```
RESULT 10
AAF64421
ID AAF64421 standard; cDNA; 393 BP.
XX
AC AAF64421;
XX
DT 09-APR-2001 (first entry)
XX
DE Novel human polynucleotide, SEQ ID NO: 177.
XX
KW Human; cytostatic; gene therapy; colon cancer; prostate cancer;
KW breast cancer; lung cancer; cancer detection; ss.
XX
OS Homo sapiens.
XX
PN WO200102568-A2.
XX
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US018374.
XX
PR 02-JUL-1999; 99US-0142310P.
PR 02-JUL-1999; 99US-0142311P.
XX
PA (CHIR ) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;
PI Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G;
PI Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
XX
DR WPI; 2001-091805/10.
XX
PT Library of polynucleotides for diagnosing a cancerous state of a
PT mammalian cell and detecting cancer, particularly of the colon or
PT prostate, comprises 3351 human polynucleotide sequences.
XX
PS Claim 9; Page 570; 1046pp; English.
XX
CC The present sequence is one of 3351 sequences in a library of human
CC polynucleotides. The library is used to detect differentially expressed
CC genes correlated with a cancerous state of a mammalian cell and can
CC detect colon, prostate, breast and lung cancer. The library can be used
CC to produce probes for detection of mRNA and to produce additional copies
CC of the polynucleotides. The probes can be used for chromosome mapping of
CC the polynucleotide and for detection of transcription levels. Ribozymes
CC or antisense oligonucleotides can be generated. The polynucleotides and
CC their gene products are used as genetic or biochemical markers (e.g. in
CC blood or tissues) that will detect the earliest changes along the
CC carcinogenesis pathway and/or monitor the efficacy of therapies and
CC preventive interventions. The polynucleotides, polypeptides and
CC antibodies against them can be used in pharmaceutical compositions to
CC treat the cancers and proliferative disorders such as neoplasia,
CC dysplasia and hyperplasia
XX
SQ Sequence 393 BP; 88 A; 122 C; 115 G; 67 T; 0 U; 1 Other;
Query Match 19.5%; Score 334; DB 5; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.1e-149; Mismatches 0; Gaps 0;
Matches 334; Conservative 0; Indels 0;

QY 805 CTGAGAGAGACAGTAAGATCTCGGACCTTATCAGCAGCATCACCGAGACTTACCACCTG 864
DB 21 CTGAGAGAGACAGTAAGATCTCGGACCTTATCAGCAGCATCACCGAGACTTACCACCTG 80
QY 865 GATGAGCAGGATGCTGAGGGCGGCTGTGATCGCGGCATCTTCGATTAGTACCCGAAAG 924
DB 81 GATGAGCAGGATGCTGAGGGCGGCTGTGATCGCGGCATCTTCGATTAGTACCCGAAAG 140
QY 925 AGCCGTGCTCGCCACAGACCTCGGAGGGTGGTTCAACTCGGGCTGCGCCACCGCT 984
DB 141 AGCCGTGCTCGCCACAGACCTCGGAGGGTGGTTCAACTCGGGCTGCGCCACCGCT 200
```

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QY 985 GCTGCCCTTGACAGTGGCCATGAGACCATGTGTGGGCTCAGTCTCAGCCAGGATGAGCTG 1044
DB 201 GCTGCCCTTGACAGTGGCCATGAGACCATGTGTGGGCTCAGTCTCAGCCAGGATGAGCTG 260
QY 1045 ACAGTGCAGATCTCCAGGAGACGACTGCAGATGCATGCGCCGAGCTGAGGCTTAT 1104
DB 261 ACAGTGCAGATCTCCAGGAGACGACTGCAGATGCATGCGCCGAGCTGAGGCTTAT 320
QY 1105 GGAGTCCAGGTTACCCAGCAAGCCATGACTCAT 1138
DB 321 GGAGTCCAGGTTACCCAGCAAGCCATGACTCAT 354

RESULT 11
AAF66376
ID AAF66376 standard; cDNA; 427 BP.
XX
AC AAF66376;
XX
DT 09-APR-2001 (first entry)
XX
DE Novel human polynucleotide, SEQ ID NO: 2132.
XX
KW Human; cytostatic; gene therapy; colon cancer; prostate cancer;
KW breast cancer; lung cancer; cancer detection; ss.
XX
OS Homo sapiens.
XX
PN WO200102568-A2.
XX
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US018374.
XX
PR 02-JUL-1999; 99US-0142310P.
PR 02-JUL-1999; 99US-0142311P.
XX
PA (CHIR ) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;
PI Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G;
PI Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
XX
DR WPI; 2001-091805/10.
XX
PT Library of polynucleotides for diagnosing a cancerous state of a
PT mammalian cell and detecting cancer, particularly of the colon or
PT prostate, comprises 3351 human polynucleotide sequences.
XX
PS Claim 9; Page 854; 1046pp; English.
XX
CC The present sequence is one of 3351 sequences in a library of human
CC polynucleotides. The library is used to detect differentially expressed
CC genes correlated with a cancerous state of a mammalian cell and can
CC detect colon, prostate, breast and lung cancer. The library can be used
CC to produce probes for detection of mRNA and to produce additional copies
CC of the polynucleotides. The probes can be used for chromosome mapping of
CC the polynucleotide and for detection of transcription levels. Ribozymes
CC or antisense oligonucleotides can be generated. The polynucleotides and
CC their gene products are used as genetic or biochemical markers (e.g. in
CC blood or tissues) that will detect the earliest changes along the
CC carcinogenesis pathway and/or monitor the efficacy of therapies and
CC preventive interventions. The polynucleotides, polypeptides and
CC antibodies against them can be used in pharmaceutical compositions to
CC treat the cancers and proliferative disorders such as neoplasia,
CC dysplasia and hyperplasia
XX
SQ Sequence 427 BP; 69 A; 161 C; 123 G; 73 T; 0 U; 1 Other;
Query Match 18.7%; Score 321; DB 5; Length 427;
```

[illegible]

RESULT 12	
AAZ13392	
ID	AAZ13392 standard; cDNA; 300 BP.
XX	
XX	AAZ13392;
XX	
DT	12-OCT-1999 (first entry)
DT	
DE	Human gene expression product cDNA sequence SEQ ID NO:861.
XX	
XX	Human; gene; gene expression product; diagnosis; therapy; probe;
KW	detection; mapping; tissue typing; profiling; forensic; cancer;
KW	genetic analysis; Colorectal cancer; breast cancer; lung cancer; ss.
XX	
XX	Homo sapiens.
OS	
XX	WO938972-A2.
PN	
XX	
XX	05-AUG-1999.
PD	
XX	
XX	28-JAN-1999; 99WO-US001619.
PF	
XX	
XX	28-JAN-1998; 98US-0072910P.
PR	
XX	24-FEB-1998; 98US-0075954P.
PR	
XX	31-MAR-1998; 98US-0080114P.
PR	
XX	03-APR-1998; 98US-0080515P.
PR	
XX	03-APR-1998; 98US-0080566P.
PR	
XX	21-OCT-1998; 98US-0105234P.
PR	
XX	28-OCT-1998; 98US-0105877P.
PA	
XX	(CHIR) CHIRON CORP.
PA	
XX	(HYSE-) HYSEQ INC.
XX	
PI	Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
XX	Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI	Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI	Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX	
DR	WPI; 1999-494092/41.
XX	
XX	Novel human genes and their expression products which are differentially
PT	expressed in different cell types.
PT	
XX	Claim 1; Page 860; 2479pp; English.
PS	
XX	
XX	

The present invention describes a library of human polynucleotides comprising the sequences given in AA212532 to AA217779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AA212532 to AA217779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists

Sequence 300 BP: 63 A; 96 C; 90 G; 51 T; 0 U; 0 Other;

Seq	Sequence	300 BP;	63 A;	96 C;	90 G;	51 T;	0 U;	0 Other;	
	Query Match	17.5%;	Score 300;	DB 2;	Length 300;				
	Best Local Similarity	100.0%;	Pred. No. 2.5e-133;						
	Matches 300;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
Qy	825	CTCGGACCTTATCAGCAGCATC	ACGCAAGGACTAC	CACCTGGATGAGCAGGATGCTGAGGG	884				
Qy	885	CCGCCTGGTACGCGGCGATCA	TTGCGATTAGTACCGGAAAGACGCGTGCTGCCCCACAGAC	944					
Qy	945	CTCGGAGGTCGTTCAACTCGGCGTGCTGCCCAACCGCTGTCGCCCTGCACAGTGCCCA	1004						
Qy	1005	TGACACCATCGGTGGGCTCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCCCAGGA	1064						
Qy	1065	GACGACTGCAGATGCCATCGCCCGGAAGCTGAGCGCTTATGGAGCTCCAGGGTACCCGAC	1124						

RESULT 13	
AAx98308	
ID	AAx98308 standard; cDNA; 300 BP.
XX	
XX	
XX	AAx98308;
XX	
DT	24-SEP-1999 (first entry)
XX	
XX	
DE	Human Cancer cell derived cDNA #34.

XX	PD	08-JUL-1999.
XX	PB	22-DEC-1998; 98WO-US027610.
XX	PF	23-DEC-1997; 97US-0068755P.
XX	PR	03-APR-1998; 98US-0080664P.
PR	PR	21-OCT-1998; 98US-0105234P.
PR	PR	27-OCT-1998; 98US-0105877P.
PR	PR	21-DEC-1998; 98US-00217471.
PA	PA	(CHIR) CHIRON CORP.
PA	PA	(HYSE-) HYSEQ INC.
XX	PI	Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
XX	PI	Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI	PI	Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI	PI	Leshkowicz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
XX	XX	WPI; 1999-430243/36.
DR	DR	New isolated human polynucleotides.
XX	PT	Claim 1; Page 326; 591pp; English.
PS	PS	This invention describes novel isolated human polynucleotides obtained by
XX	CC	screening for differential expression in colon cancer, breast cancer and
CC	CC	lung cancer cell lines. The polynucleotides of the invention are
CC	CC	represented in AAX98275-X99118 and encode polypeptides of protein
CC	CC	families selected from 4 transmembrane segments integral membrane
CC	CC	proteins, 7 transmembrane receptors, ATPases associated with various
CC	CC	cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC	CC	transcription factors, G-protein alpha subunit, phospholipase or
CC	CC	diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
CC	CC	protein tyrosine phosphatase, trypsin, wnt family of developmental
CC	CC	signalling proteins and WW/rps5/WWP domain containing proteins. The
CC	CC	encoded polypeptides also have a functional domain selected from Ank
CC	CC	repeat, basic region plus leucine zipper transcription factors,
CC	CC	bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger
CC	CC	(C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease
CC	CC	domain. The polynucleotides encode polypeptides with similarity to known
CC	CC	protein families and are predicted to have similar properties. The novel
CC	CC	polynucleotides can be used to develop products for use as therapeutic
CC	CC	agents and in forensics, genetic analysis, mapping and diagnostic
CC	CC	applications. In particular, the product can be used for the detection
CC	CC	and management of cancers. They can be used for treating e.g. cervical
CC	CC	cancers, melanomas, colorectal adenocarcinomas, Wilms tumour, sarcomas,
CC	CC	retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
CC	CC	myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
CC	CC	myeloid leukemia, and lymphomas such as histiocytic lymphoma, anhydric
CC	CC	hereditary ectodermal dysplasia, congenital alveolar dysplasia,
CC	CC	epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
CC	CC	mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
CC	CC	prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC	CC	the skin
XX	XX	
SQ	SQ	Sequence 300 BP; 68 A; 90 C; 86 G; 56 T; 0 U; 0 Other;
Query Match 14.5%; Score 249; DB 2; Length 300;		
Best Local Similarity 99.7%; Pred. No. 7.9e-109;		
Matches 299; Conservative 0; Mismatches -1; Indels 0; Gaps 0		
QY	740	TGACAGAGCTGTTCAGCGCTACACAGATCGATGAGTCTCGGACCTTTATCAGCAGCATCACGCAGACTGG 799
Dd		
Dd	1	TGACAGAGCTGTTTGAGCGCTACACAGATCGATGAGTCTCGGACCTTTATCAGCAGCATCACGCAGACTGG 60
QY	800	TGTTTCTCGGAAGACCAGTAGTAAGATCTCGGACCTTTATCAGCAGCATCACGCAGGACTACC 859
Dd		
Dd	61	TGTTTCTCGGAAGACCAGTAGTAAGATCTCGGACCTTTATCAGCAGCATCACGCAGGACTACC 120
QY	860	ACCTGGATGACACGATGCTGAGGGCCGCCCTGGTACGGCGCATCATTCGCAATTAGTACC 919
Dd		
Dd	121	ACCTGGATGACACGATGCTGAGGGCCGCCCTGGTACGGCGCATCATTCGCAATTAGTACC 180


```
AC AAH69926;
XX
XX 19-SEP-2001 (first entry)
XX
XX Human cervical cancer marker nucleic acid 1200.
XX
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX WO200142467-A2.
XX
XX 14-JUN-2001.
XX
XX 08-DEC-2000; 2000WO-US033312.
XX
XX 08-DEC-1999; 99US-0169681P.
XX
XX 21-DEC-1999; 99US-0171350P.
XX
XX 14-MAR-2000; 2000US-0189315P.
XX
XX 12-MAY-2000; 2000US-0203791P.
XX
XX 09-JUN-2000; 2000US-0210600P.
XX
XX 21-JUL-2000; 2000US-0220114P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Deeds J, Berger A, Zhao X;
PI
XX WPI; 2001-375006/39.
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
PT for assessing and detecting compounds for treating the cancer.
XX
XX Claim 1; Page 294; 1051pp; English.
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy
XX
XX Sequence 323 BP; 92 A; 71 C; 76 G; 84 T; 0 U; 0 Other;
SQ
    Query Match      1.6%; Score 28; DB 4; Length 323;
    Best Local Similarity 100.0%; Pred. No. 0.012;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 1686 TTTGTAAGTACCTCGCGCGGACACGC 1713
    Db 34 TTTGTAAGTACCTCGCGCGGACACGC 7

RESULT 18
AAH69438/c
ID AAH69438 standard; cDNA; 329 BP.
XX
XX AAH69438;
XX
XX 19-SEP-2001 (first entry)
XX
XX Human cervical cancer marker nucleic acid 712.
XX
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX WO200142467-A2.
XX
XX 14-JUN-2001.
XX
XX 08-DEC-2000; 2000WO-US033312.
XX
XX
```

```
XX 08-DEC-1999; 99US-0169681P.
XX
XX 21-DEC-1999; 99US-0171350P.
XX
XX 14-MAR-2000; 2000US-0189315P.
XX
XX 12-MAY-2000; 2000US-0203791P.
XX
XX 09-JUN-2000; 2000US-0210600P.
XX
XX 21-JUL-2000; 2000US-0220114P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Deeds J, Berger A, Zhao X;
PI
XX WPI; 2001-375006/39.
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
PT for assessing and detecting compounds for treating the cancer.
XX
XX Claim 1; Page 226; 1051pp; English.
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy
XX
XX Sequence 329 BP; 106 A; 45 C; 59 G; 119 T; 0 U; 0 Other;
SQ
    Query Match      1.6%; Score 28; DB 4; Length 329;
    Best Local Similarity 100.0%; Pred. No. 0.012;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 1686 TTTGTAAGTACCTCGCGCGGACACGC 1713
    Db 34 TTTGTAAGTACCTCGCGCGGACACGC 7

RESULT 19
AAH98612/c
ID AAH98612 standard; DNA; 91 BP.
XX
XX AAH98612;
XX
XX 02-JUL-2001 (first entry)
XX
XX Human ovarian cancer cell expressed sequence 3785.
XX
XX Human; ovarian cancer; identification; detection; characterisation;
XX tumour; kinase; marker; cytostatic; antisense gene therapy; ds.
XX
XX Homo sapiens.
OS
XX WO200118542-A2.
XX
XX 15-MAR-2001.
XX
XX 01-SEP-2000; 2000WO-US024199.
XX
XX 03-SEP-1999; 99US-0152547P.
XX
XX 16-MAR-2000; 2000US-0190347P.
XX
XX 21-MAR-2000; 2000US-0191321P.
XX
XX 31-MAY-2000; 2000US-0208382P.
XX
XX 20-JUL-2000; 2000US-00220467.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Thompson P, Lillie J;
PI
XX WPI; 2001-211428/21.
XX
XX Detection, assessment, prevention and therapy of ovarian cancer,
XX
```

PT comprises detecting changes in the expression of a variety of markers.
XX
XX Claim 1; Page 988; 1190pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with ovarian cancer by comparing: (1) the expression of a
CC marker (I) (see AAF98594 to AAF98730), in a patient sample; and (2) the
CC normal level of expression of (I) in a control non-ovarian cancer sample,
CC where a significant difference between the level of expression in (a) and
CC (b) is an indication that the patient is afflicted with ovarian cancer.
CC (I) have cytostatic activities and can be used in antisense gene therapy.
CC The method, compositions and kits from the present invention can be used
CC for: (1) assessing and treating ovarian cancer; (2) making isolated
CC hybridoma, which produces an antibody useful for ovarian cancer
CC assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to
CC AAF98593 represent human kinase marker primers and probes which are used
CC in the exemplification of the present invention
XX
XX Sequence 91 BP; 23 A; 17 C; 20 G; 31 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 26; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1688 TGTAAGTACCTCGCGCGGACACGC 1713
Db 32 TGTAAGTACCTCGCGCGGACACGC 7
RESULT 20
ID AAH70084 standard; cDNA; 203 BP.
XX
XX AAH70084;
AC
XX
XX 19-SEP-2001 (first entry)
DT
XX
XX Human cervical cancer marker nucleic acid 1358.
DE
XX
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200142467-A2.
PN
XX
XX 14-JUN-2001.
FD
XX
XX 08-DEC-2000; 2000WO-US033312.
FF
XX
XX 08-DEC-1999; 99US-0169681P.
PR
XX
XX 21-DEC-1999; 99US-0171350P.
PR
XX
XX 14-MAR-2000; 2000US-0189315P.
PR
XX
XX 12-MAY-2000; 2000US-0203791P.
PR
XX
XX 09-JUN-2000; 2000US-0210600P.
PR
XX
XX 21-JUL-2000; 2000US-0220114P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX Schlegel R, Deeds J, Berger A, Zhao X;
PI
XX
XX WPI; 2001-375006/39.
DR
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
XX for assessing and detecting compounds for treating the cancer.
PT
XX
XX Claim 1; Page 314; 1051pp; English.
PS
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX polypeptides are useful: to assess if a patient is afflicted with
XX cervical cancer or has a pre-malignant condition; to monitor the
XX progression of cervical cancer or a premalignant condition in a patient;
XX and to select and/or assess the efficacy of a compound or therapy for

CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy
XX
XX Sequence 203 BP; 52 A; 41 C; 59 G; 51 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 26; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1688 TGTAAGTACCTCGCGCGGACACGC 1713
Db 32 TGTAAGTACCTCGCGCGGACACGC 7
RESULT 21
ID AAH70907 standard; cDNA; 412 BP.
XX
XX AAH70907;
AC
XX
XX 19-SEP-2001 (first entry)
DT
XX
XX Human cervical cancer marker nucleic acid 2181.
DE
XX
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200142467-A2.
PN
XX
XX 14-JUN-2001.
PD
XX
XX 08-DEC-2000; 2000WO-US033312.
PE
XX
XX 08-DEC-1999; 99US-0169681P.
PR
XX
XX 21-DEC-1999; 99US-0171350P.
PR
XX
XX 14-MAR-2000; 2000US-0189315P.
PR
XX
XX 12-MAY-2000; 2000US-0203791P.
PR
XX
XX 09-JUN-2000; 2000US-0210600P.
PR
XX
XX 21-JUL-2000; 2000US-0220114P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX Schlegel R, Deeds J, Berger A, Zhao X;
PI
XX
XX WPI; 2001-375006/39.
DR
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
XX for assessing and detecting compounds for treating the cancer.
PT
XX
XX Claim 1; Page 461; 1051pp; English.
PS
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX polypeptides are useful: to assess if a patient is afflicted with
XX cervical cancer or has a pre-malignant condition; to monitor the
XX progression of cervical cancer or a premalignant condition in a patient;
XX and to select and/or assess the efficacy of a compound or therapy for
XX inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy
SQ
Sequence 412 BP; 125 A; 77 C; 83 G; 127 T; 0 U; 0 Other;
Query Match 1.5%; Score 26; DB 4; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1686 TTGTAAAGTACCTCGCGCGGACACGC 1711
Db 377 TTGTAAAGTACCTCGCGCGGACACGC 402
RESULT 22

```
AA117411
ID AAL17411 standard; cDNA; 576 BP.
XX
AC AAL17411;
XX
XX 07-DEC-2001 (first entry)
DT
DE Human breast cancer expressed polynucleotide 9868.
XX
XX Human; breast cancer; cell marker; cytostatic; ss.
XX
XX Homo sapiens.
XX
XX WO200151628-A2.
XX
XX 19-JUL-2001.
XX
XX 10-JAN-2001; 2001WO-US000798.
XX
XX 14-JAN-2000; 2000US-0176077P.
XX
XX 14-MAR-2000; 2000US-0189167P.
XX
XX 24-MAR-2000; 2000US-0192099P.
XX
XX 29-MAR-2000; 2000US-0193480P.
XX
XX 15-MAY-2000; 2000US-0205230P.
XX
XX 09-JUN-2000; 2000US-0211315P.
XX
XX 25-JUL-2000; 2000US-0220534P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX
XX WPI; 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer.
XX
XX Claim 1; Page 1758; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AA126789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity
XX
XX Sequence 576 BP; 134 A; 111 C; 125 G; 205 T; 0 U; 1 Other;
SQ
Query Match 1.5%; Score 26; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1688 TGTAGTACTCGCGCGGACCAACGC 1713
DB 550 TGTAGTACTCGCGCGGACCAACGC 575
RESULT 23
ABZ08482
ID ABZ08482 standard; cDNA; 224 BP.
XX
XX ABZ08482;
XX
XX 09-JAN-2003 (first entry)
DT
DE Human leukocyte derived cDNA SEQ ID NO 8473.
XX
XX Human; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; gene;
XX ss.
XX
OS Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX
XX 16-MAR-2000; 2000US-0189862P.
XX
OS Homo sapiens.
XX
XX WO200257414-A2.
XX
XX 25-JUL-2002.
XX
XX 22-OCT-2001; 2001WO-US047856.
XX
XX 20-OCT-2000; 2000US-0241994P.
XX
XX 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quertermous T, Johnson F;
XX
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 26; Page 1920; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection. The
XX present sequence is that of a human leukocyte expressed cDNA of the
XX invention
XX
XX Sequence 224 BP; 80 A; 44 C; 44 G; 44 T; 0 U; 12 Other;
SQ
Query Match 1.5%; Score 25; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1689 GTAAGTACTCGCGCGGACCAACGC 1713
DB 189 GTAAGTACTCGCGCGGACCAACGC 213
RESULT 24
ABV37465/c
ID ABV37465 standard; cDNA; 255 BP.
XX
XX ABV37465;
XX
XX 16-SEP-2002 (first entry)
DT
DE Human prostate expression marker cDNA 37456.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX
XX 16-MAR-2000; 2000US-0189862P.
XX
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PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX PS Claim 1; Page 7689; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy
XX of progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 255 BP; 56 A; 55 C; 80 G; 64 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 5; Length 255;
XX Best Local Similarity 100.0%; Pred. No. 0.34;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1689 GTAAGTACTCGCGCGACACGC 1713
XX |||||||
XX DB 97 GTAAGTACTCGCGCGACACGC 73
XX
XX RESULT 25
XX ADL43520/c
XX ID ADL43520 standard; DNA; 275 BP.
XX
XX AC ADL43520;
XX
XX XX 20-MAY-2004 (first entry)
XX
XX XX Human ovarian cancer DNA marker #17410.
XX
XX XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX OS Homo sapiens.
XX
XX PN WO200170979-A2.
XX
XX XX 27-SEP-2001.
XX
XX XX 21-MAR-2001; 2001WO-US009126.
XX
XX XX 21-MAR-2000; 2000US-0191031P.
XX
XX PR 25-MAY-2000; 2000US-0207124P.
XX
XX FR 15-JUN-2000; 2000US-0211940P.
XX
XX PR 07-JUL-2000; 2000US-0216820P.
XX
XX PR 25-JUL-2000; 2000US-0220661P.
XX
XX PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX PI Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX
XX DR
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XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX PS Disclosure; SEQ ID NO 17410; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX
XX SQ Sequence 275 BP; 71 A; 64 C; 71 G; 69 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 5; Length 275;
XX Best Local Similarity 100.0%; Pred. No. 0.34;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1689 GTAAGTACTCGCGCGACACGC 1713
XX |||||||
XX DB 87 GTAAGTACTCGCGCGACACGC 63
XX
XX RESULT 26
XX ABV07533/c
XX ID ABV07533 standard; cDNA; 304 BP.
XX
XX AC ABV07533;
XX
XX XX 13-SEP-2002 (first entry)
XX
XX XX Human prostate expression marker cDNA 7524.
XX
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200160860-A2.
XX
XX XX 23-AUG-2001.
XX
XX XX 20-FEB-2001; 2001WO-US005171.
XX
XX XX 17-FEB-2000; 2000US-0183319P.
XX
XX PR 16-MAR-2000; 2000US-0189862P.
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PR 09-JUN-2000; 2000US-0210600P.
XX 21-JUL-2000; 2000US-0220114P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Deede J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
XX for assessing and detecting compounds for treating the cancer.
XX Claim 1; Page 264; 1051pp; English.
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX polypeptides are useful: to assess if a patient is afflicted with
XX cervical cancer or has a pre-malignant condition; to monitor the
XX progression of cervical cancer or a premalignant condition in a patient;
XX and to select and/or assess the efficacy of a compound or therapy for
XX inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy
XX
XX Sequence 359 BP; 92 A; 57 C; 74 G; 135 T; 0 U; 1 Other;
SQ
Query Match 1.5%; Score 25; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1689 GTAAGTACCTCGGCGGACACCG 1713
DB 31 GTAAGTACCTCGGCGGACACCG 7
RESULT 31
ABV98985
ID ABV98985 standard; cDNA; 453 BP.
XX
AC ABV98985;
XX
XX 14-JAN-2003 (first entry)
XX Human pancreatic cancer expressed cDNA SEQ ID NO 4393.
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX cytostatic; tumour; gene; ss.
XX Homo sapiens.
XX WO200260317-A2.
XX
XX 08-AUG-2002.
XX
XX 30-JAN-2002; 2002WO-US002781.
XX
XX 30-JAN-2001; 2001US-0265305P.
XX 31-JAN-2001; 2001US-0265682P.
XX 09-FEB-2001; 2001US-0267568P.
XX 21-MAR-2001; 2001US-0278651P.
XX 28-APR-2001; 2001US-0287112P.
XX 16-MAY-2001; 2001US-0291631P.
XX 12-JUL-2001; 2001US-0305484P.
XX 20-AUG-2001; 2001US-0313999P.
XX 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
XX diagnosing, preventing and/or treating cancer, particularly pancreatic
PT
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PT cancer.
XX Claim 1; SEQ ID NO 4393; 300pp + Sequence Listing; English.
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
XX complements of (a); (c) sequences consisting of at least 20 contiguous
XX residues of (a); (d) sequences that hybridize to (a), under moderately
XX stringent conditions; (e) sequences having at least 75% or 90% identity
XX to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
XX ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
XX in a patient and compositions comprising polypeptides, polynucleotides,
XX antibodies, fusion proteins, T cell populations and antigen presenting
XX cells expressing the polypeptide are useful in treating pancreatic cancer
XX and stimulating an immune response. The polynucleotides can be used as
XX probes or primers for nucleic acid hybridisation, in the design and
XX preparation of ribozyme molecules for inhibiting expression of the tumour
XX polypeptides and proteins in the tumour cells, in vaccines and for gene
XX therapy. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 453 BP; 100 A; 93 C; 131 G; 129 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1689 GTAAGTACCTCGGCGGACACCG 1713
DB 428 GTAAGTACCTCGGCGGACACCG 452
RESULT 32
ADL43881
ID ADL43881 standard; DNA; 463 BP.
XX
AC ADL43881;
XX
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #17771.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 17771; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX
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ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 1.5%; Score 25; DB 5; Length 463; Best Local Similarity 100.0%; Pred. No. 0.34; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAGTACCTCGCGCGACACGC 1713
Db 351 GTAAAGTACCTCGCGCGACACGC 375

RESULT 33
ABS67274/c
ID ABS67274 standard; cDNA; 810 BP.

AC ABS67274;
XX
XX 29-NOV-2002 (first entry)
XX Breast specific polynucleotide #10.
DE
XX Breast specific; cancer staging; cancer imaging; breast cancer;
KW non-cancerous disease states in breast tissue; gene therapy; vaccine;
KW transgenic animal; gene; ss.
XX
XX Homo sapiens.

OS
XX
XX WO200264741-A2.
XX
XX 22-AUG-2002.
XX

XX 12-FEB-2002; 2002WO-US004134.
XX
XX 13-FEB-2001; 2001US-0268289P.
XX (DIAD-) DIADEXUS INC.

XX Salceda S, Macina RA, Hu P, Recipon H, Karra K, Cafferkey R;
PI Liu C, Sun Y;

DR WPI; 2002-657590/70.

XX New breast specific nucleic acids and proteins, for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, or for gene therapy.
XX Claim 1; Page 156; 227pp; English.

XX The invention describes a breast specific nucleic acid. The nucleic acids, polypeptides, antibodies, agonists and antagonists, and compositions comprising them are useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, in gene therapy, vaccine development, in producing transgenic animals and cells, and in producing engineered breast tissue for treatment and research. The nucleic acids may be used as molecular markers for detecting breast cancer for accurate staging of the disease and monitoring the progress of cancer treatments, and as hybridisation probes or primers. This sequence encodes a breast specific protein of the invention

Query Match 1.5%; Score 25; DB 6; Length 810; Best Local Similarity 100.0%; Pred. No. 0.34; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 GTAGTACCTCGCGCGACACGC 1713
Db 25 GTAAAGTACCTCGCGCGACACGC 1

RESULT 34
ACN84455/c
ID ACN84455 standard; DNA; 1252 BP.

XX ACN84455;
XX 02-DEC-2004 (first entry)
XX Breast cancer related marker, seq id 5605.
DE
XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
KW
XX Homo sapiens.

OS
XX US2003099974-A1.
XX 29-MAY-2003.
XX

XX 18-JUL-2002; 2002US-00198846.
XX 18-JUL-2001; 2001US-0306220P.
XX (MTLL-) MILLENNIUM PHARM INC.

XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI WPI; 2003-787014/74.

XX Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast cancer.

XX Disclosure; SEQ ID NO 5605; 36pp; English.

XX The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given

CC be used in gene therapy for treating disorders. This sequence represents
CC an immune-related mouse protein of the invention. This polynucleotide
CC represents an immune-related mouse DNA sequence of the invention

XX Sequence 232 BP; 52 A; 43 C; 49 G; 86 T; 0 U; 2 Other;

Query Match 1.4%; Score 24; DB 8; Length 232;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1698 TGTAAGTACCTCGCGCGGACAC 1711

|||||

Db 207 TGTAAGTACCTCGCGCGGACAC 230

RESULT 37

ADL43332/c

ID ADL43332 standard; DNA; 253 BP.

XX

AC ADL43332;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human ovarian cancer DNA marker #17222.

XX

KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX

OS Homo sapiens.

XX

FN WO200170979-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US009126.

XX

PR 21-MAR-2000; 2000US-0191031P.

XX

PR 25-MAY-2000; 2000US-0207124P.

XX

PR 15-JUN-2000; 2000US-0211940P.

XX

PR 07-JUL-2000; 2000US-0216820P.

XX

PR 25-JUL-2000; 2000US-0220661P.

XX

PR 21-DEC-2000; 2000US-0257672P.

XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

PI Lee J, Lillie J;

XX

XX WPI; 2001-611502/70.

DR

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

XX cancer cells as compared to their normal non-cancerous ovarian cells are

XX used to characterize stage, grade, histological type of ovarian cancer.

XX

PS Disclosure; SEQ ID NO 17222; 106pp; English.

XX

CC The invention relates to nucleic acid markers which are overexpressed in

CC ovarian cancer cells as compared to their expression in normal (i.e. non-

CC cancerous) ovarian cells. The invention also relates to polypeptides

CC encoded by the markers, antibodies that selectively bind to the

CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk

CC of developing ovarian cancer involving inhibiting expression of a gene

CC corresponding to a marker of the invention and a method of treating a

CC patient afflicted with ovarian cancer comprising providing to cells of

CC the patient an antisense oligonucleotide complementary to a marker of the

CC invention. The markers are useful for assessing if a patient is afflicted

CC with ovarian cancer, which involves comparing the level of expression of

CC a marker in a patient sample and a normal level of expression of the

CC marker in a control non-ovarian cancer sample. A difference between the

CC expression levels indicates ovarian cancer. The level of expression of a

CC marker corresponds to a secreted protein or to a transcribed

CC polynucleotide or its portion. The level of expression of the marker is

CC assessed by detecting the presence in the sample, a protein or protein

CC fragment corresponding to the marker. The presence of protein or protein

CC fragment is detected using an antibody that specifically binds with the

CC protein or protein fragment. Alternatively, the level of expression of

CC the marker is assessed by detecting the presence of a transcribed

CC polynucleotide which anneals with the marker or anneals with a portion of

CC the polynucleotide comprising the marker, under stringent conditions. The

CC marker is also used for monitoring the progression of ovarian cancer in a

CC patient which involves detecting expression of the marker in a patient

CC sample at a first point in time, repeating the method at a subsequent

CC time and comparing the level of expression. The method is carried out

CC using an ovarian tissue sample. A composition comprising a marker,

CC polypeptide or antibody of the invention is used to treat ovarian cancer.

CC This sequence represents a human ovarian cancer DNA marker of the

CC invention.

SQ Sequence 253 BP; 44 A; 65 C; 65 G; 79 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 253;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713

|||||

Db 77 TAAGTACCTCGCGCGGACACGC 54

RESULT 38

ADL37742/c

ID ADL37742 standard; DNA; 274 BP.

XX

AC ADL37742;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human ovarian cancer DNA marker #11632.

XX

KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX

OS Homo sapiens.

XX

FN WO200170979-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US009126.

XX

PR 21-MAR-2000; 2000US-0191031P.

XX

PR 25-MAY-2000; 2000US-0207124P.

XX

PR 15-JUN-2000; 2000US-0211940P.

XX

PR 07-JUL-2000; 2000US-0216820P.

XX

PR 25-JUL-2000; 2000US-0220661P.

XX

PR 21-DEC-2000; 2000US-0257672P.

XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

PI Lee J, Lillie J;

XX

XX WPI; 2001-611502/70.

DR

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

XX cancer cells as compared to their normal non-cancerous ovarian cells are

XX used to characterize stage, grade, histological type of ovarian cancer.

XX

PS Disclosure; SEQ ID NO 11632; 106pp; English.

XX

CC The invention relates to nucleic acid markers which are overexpressed in

CC ovarian cancer cells as compared to their expression in normal (i.e. non-

CC cancerous) ovarian cells. The invention also relates to polypeptides

CC encoded by the markers, antibodies that selectively bind to the

CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk

CC of developing ovarian cancer involving inhibiting expression of a gene

CC corresponding to a marker of the invention and a method of treating a

CC patient afflicted with ovarian cancer comprising providing to cells of

CC the patient an antisense oligonucleotide complementary to a marker of the

CC invention. The markers are useful for assessing if a patient is afflicted

PI Lee J, Lillie J;
DR WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 16395; 106pp; English.
PS
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 283 BP; 94 A; 62 C; 50 G; 77 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 283;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713
Db |||||||||||||||||||
54 TAAGTACTCGCGCGGACACGC 31

RESULT 41
ADI70936/c
ID ADI70936 standard; DNA; 310 BP.
XX
XX ADI70936;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human ovarian cancer DNA marker #3678.
DE
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
KW
XX Homo sapiens.
OS
XX WO200170979-A2.
PN
XX 27-SEP-2001.
XX
XX

PF 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 3678; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.
XX
SQ Sequence 310 BP; 72 A; 54 C; 66 G; 118 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACACGC 1713
Db |||||||||||||||||||
30 TAAGTACTCGCGCGGACACGC 7

RESULT 42
ADI77249/c
ID ADI77249 standard; DNA; 310 BP.
XX
XX ADI77249;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human ovarian cancer DNA marker #9991.
DE

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
KW Homo sapiens.
OS WO200170979-A2.
PN 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 9991; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 310 BP; 72 A; 54 C; 66 G; 118 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACCGC 1713
|||||
DB 30 TAAGTACCTCGCGCGACCGC 7

RESULT 43
ADL36491/C
ID ADL36491 standard; DNA; 312 BP.
XX AC ADL36491;
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #10381.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
KW Homo sapiens.
OS WO200170979-A2.
PN 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 10381; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 312 BP; 99 A; 53 C; 47 G; 113 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACCCAGC 1713
Db 30 TAAGTACTCGCGCGGACCCAGC 7

RESULT 45
ADI71332/C
ID ADI71332 standard; DNA; 312 BP.
XX
AC ADI71332;
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #4074.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 4074; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed

CC polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention.
XX
SQ Sequence 312 BP; 99 A; 53 C; 47 G; 113 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGGACCCAGC 1713
Db 30 TAAGTACTCGCGCGGACCCAGC 7

RESULT 45
ADI70234/C
ID ADI70234 standard; DNA; 319 BP.
XX
AC ADI70234;
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #2976.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 2976; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the

CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX Sequence 319 BP; 77 A; 61 C; 78 G; 99 T; 0 U; 4 Other;

Query Match 1.4%; Score 24; DB 5; Length 319;

Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTCGCGCGACACGC 1713

Db 30 TAAGTACTCTCGCGCGACACGC 7

RESULT 46

AD176563/c

ID AD176563 standard; DNA; 319 BP.

XX

AC AD176563;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human ovarian cancer DNA marker #9305.

XX

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX

OS Homo sapiens.

XX

PN WO200170979-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US009126.

XX

PR 21-MAR-2000; 2000US-0191031P.

XX

PR 25-MAY-2000; 2000US-0207124P.

XX

PR 15-JUN-2000; 2000US-0211940P.

XX

PR 07-JUL-2000; 2000US-0216820P.

XX

PR 25-JUL-2000; 2000US-0220661P.

XX

PR 21-DEC-2000; 2000US-0257672P.

XX

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

PI Lee J, Lillie J;

XX

XX WPI; 2001-611502/70.

XX

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

PT cancer cells as compared to their normal non-cancerous ovarian cells are

PT used to characterize stage, grade, histological type of ovarian cancer.

XX

PS Disclosure; SEQ ID NO 9305; 106pp; English.

XX

CC The invention relates to nucleic acid markers which are overexpressed in

CC ovarian cancer cells as compared to their expression in normal (i.e. non-

CC cancerous) ovarian cells. The invention also relates to polypeptides

CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of the
CC patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX Sequence 319 BP; 77 A; 61 C; 78 G; 99 T; 0 U; 4 Other;

Query Match 1.4%; Score 24; DB 5; Length 319;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTCGCGCGACACGC 1713

Db 30 TAAGTACTCTCGCGCGACACGC 7

RESULT 47

ABQ58175

ID ABQ58175 standard; cDNA; 320 BP.

XX

AC ABQ58175;

XX

DT 02-AUG-2002 (first entry)

XX

DE Human colon cancer related nucleotide sequence SEQ ID NO:1870.

XX

XX Human; colon cancer; cancer; tissue profiling; forensic; mapping;

KW genetic analysis; diagnostic; antisense therapy; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200229086-A2.

XX

PD 11-APR-2002.

XX

XX 02-OCT-2001; 2001WO-US030732.

XX

XX 02-OCT-2000; 2000US-0237271P.

XX

XX (FARB) BAYER CORP.

XX

PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;

PI Thiagalingam A, Lewis ME;

XX

XX WPI; 2002-426115/45.

XX

XX New isolated nucleic acid that is differentially expressed in cancer

PT tissues useful for determining the presence of colon cancer in a cell or
 XX tissue type, and in antisense therapy.

PS Claim 1; Fig 1; 796pp; English.

XX ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
 CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
 CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
 CC used in antisense therapy. An antibody immunoreactive with a polypeptide
 CC encoded by (I) is useful for detecting cancer in a patient sample, and
 CC for detecting the presence or absence of a polynucleotide encoded by a
 CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived
 CC from (I) can be used for determining the presence of a nucleic acid which
 CC hybridizes to (I), and for determining the phenotype of cells in a sample
 CC of cells from a patient. (I) is useful for determining the presence of
 CC colon cancer in a cell or tissue type, for determining the presence or
 CC state of other type of cancer, in antisense therapy, to generate
 CC macroarrays on a solid surface, to identify a chromosome on which the
 CC corresponding gene resides, and in tissue profiling, forensics, genetic
 CC analysis, mapping and diagnostic applications. (I) can be used to raise
 CC antibodies, and to screen for peptide analogues and antagonists

XX SQ Sequence 320 BP; 66 A; 89 C; 89 G; 75 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 6; Length 320;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 289 TAAGTACTCGCGCGACACGC 312

RESULT 48

ADL44057/C

ID ADL44057 standard; DNA; 326 BP.

AC ADL44057;

XX 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #17947.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 XX cancer cells as compared to their normal non-cancerous ovarian cells are
 XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 17947; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in

CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides
 CC encoded by the markers, antibodies that selectively bind to the
 CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
 CC of developing ovarian cancer involving inhibiting expression of a gene
 CC corresponding to a marker of the invention and a method of treating a
 CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a
 CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 326 BP; 92 A; 70 C; 47 G; 116 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 5; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 113 TAAGTACTCGCGCGACACGC 90

RESULT 49

AAH69655/C

ID AAH69655 standard; cDNA; 331 BP.

XX AAH69655;

XX 19-SEP-2001 (first entry)

XX Human cervical cancer marker nucleic acid 929.

XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

XX Homo sapiens.

XX WO200142467-A2.

XX 14-JUN-2001.

XX 08-DEC-2000; 2000WO-US033312.

XX 08-DEC-1999; 99US-0169681P.

XX 21-DEC-1999; 99US-0171350P.

XX 14-MAR-2000; 2000US-0189315P.

XX 12-MAY-2000; 2000US-0203791P.

XX 09-JUN-2000; 2000US-0210600P.

XX 21-JUL-2000; 2000US-0220114P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
PT for assessing and detecting compounds for treating the cancer.
XX
XX Claim 1; Page 257-258; 1051pp; English.
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful; to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy
XX
XX Sequence 331 BP; 109 A; 49 C; 59 G; 114 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 24; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGACCGC 1713
Db 30 TAAGTACCTCGCGCGACCGC 7
RESULT 50
AAL13080/c
ID AAL13080 standard; cDNA; 337 BP.
AC AAL13080;
XX
XX 07-DEC-2001 (first entry)
DT Human breast cancer expressed polynucleotide 5537.
XX
XX Human breast cancer; cell marker; cytostatic; ss.
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
XX Homo sapiens.
OS
XX WO200151628-A2.
PN
XX 19-JUL-2001.
PD
XX 10-JAN-2001; 2001WO-US000799.
PF 14-JAN-2000; 2000US-0176077P.
PR 14-MAR-2000; 2000US-0189167P.
PR 24-MAR-2000; 2000US-0192099P.
PR 29-MAR-2000; 2000US-0193480P.
PR 15-MAY-2000; 2000US-0205230P.
PR 09-JUN-2000; 2000US-0211315P.
PR 25-JUL-2000; 2000US-0220534P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer.
PT
XX Claim 1; Page 995; 3695pp; English.
PS
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and

CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity
XX
XX Sequence 337 BP; 127 A; 63 C; 60 G; 83 T; 0 U; 4 Other;
SQ
Query Match 1.4%; Score 24; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGACCGC 1713
Db 30 TAAGTACCTCGCGCGACCGC 7
RESULT 51
AAH69708/c
ID AAH69708 standard; cDNA; 338 BP.
AC AAH69708;
XX
XX 19-SEP-2001 (first entry)
DT Human cervical cancer marker nucleic acid 982.
XX
XX Human cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
KW Homo sapiens.
OS
XX WO200142467-A2.
PN
XX 14-JUN-2001.
PD
XX 08-DEC-2000; 2000WO-US033312.
PF 08-DEC-1999; 99US-0169681P.
PR 21-DEC-1999; 99US-0171350P.
PR 14-MAR-2000; 2000US-0189315P.
PR 12-MAY-2000; 2000US-0203791P.
PR 09-JUN-2000; 2000US-0210600P.
PR 21-JUL-2000; 2000US-0220114P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer and
PT for assessing and detecting compounds for treating the cancer.
XX
XX Claim 1; Page 264; 1051pp; English.
XX
XX The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful; to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy
XX
XX Sequence 338 BP; 94 A; 64 C; 87 G; 93 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 24; DB 4; Length 338;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGACCGC 1713
Db 30 TAAGTACCTCGCGCGACCGC 7

RESULT 52
 ABV08004/c
 ID ABV08004 standard; cDNA; 346 BP.
 XX
 KW Homo sapiens.
 XX
 AC ABV08004;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 7995.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-0183319P.
 XX
 PR 16-MAR-2000; 2000US-0189862P.
 PR
 PR 25-MAY-2000; 2000US-0207454P.
 PR
 PR 09-JUN-2000; 2000US-0211314P.
 PR
 PR 18-JUL-2000; 2000US-0219007P.
 PR
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 1280; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 CC
 SQ Sequence 346 BP; 126 A; 60 C; 57 G; 103 T; 0 U; 0 Other;
 XX
 Query Match 1.4%; Score 24; DB 5; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1690 TAAGTACCTCGCGCGACACGC 1713
 ||||||||||||||||||
 DB 30 TAAGTACCTCGCGCGACACGC 7
 RESULT 53
 ADL37120/c
 ID ADL37120 standard; DNA; 368 BP.
 XX
 AC ADL37120;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human ovarian cancer DNA marker #11010.

RESULT 54
ADI171969/c
ID ADI171969 standard; DNA; 368 BP.
XX
AC ADI171969;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #4711.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Lillie J;
XX
DR WPI; 2001-611502/70.
XX
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
PS Disclosure; SEQ ID NO 4711; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQL Sequence 368 BP; 96 A; 67 C; 84 G; 120 T; 0 U; 1 Other;
Query Match 1.4%; Score 24; DB 5; Length 368;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAACTACCTCGCGCGGACCGC 1713
DB 30 TAACTACCTCGCGCGGACCGC 7
RESULT 55
ADI173216/c
ID ADI173216 standard; DNA; 370 BP.
XX
AC ADI173216;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #5958.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Lillie J;
XX
DR WPI; 2001-611502/70.
XX
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
PS Disclosure; SEQ ID NO 5958; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The

CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX Sequence 370 BP; 131 A; 76 C; 61 G; 96 T; 0 U; 6 Other;

Query Match 1.4%; Score 24; DB 5; Length 370;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 56

ADL38348/c

ID ADL38348 standard; DNA; 370 BP.

XX AC ADL38348;

XX DT 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #12238.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-02071124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 12238; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a

CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX Sequence 370 BP; 131 A; 76 C; 61 G; 96 T; 0 U; 6 Other;

Query Match 1.4%; Score 24; DB 5; Length 370;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 57

ABV06075/c

ID ABV06075 standard; cDNA; 376 BP.

XX AC ABV06075;

XX DT 13-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 6066.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

XX 17-FEB-2000; 2000US-0183319P.

XX 16-MAR-2000; 2000US-0189852P.

XX 25-MAY-2000; 2000US-0207454P.

XX 09-JUN-2000; 2000US-0211314P.

XX 18-JUL-2000; 2000US-0219007P.

XX 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 1006; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the

CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX

Sequence 376 BP; 122 A; 55 C; 63 G; 136 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 376;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713

Db 30 TAAGTACCTCGCGCGACACGC 7
 |||||

RESULT 58

ADL42875/c

ID ADL42875 standard; DNA; 382 BP.

XX

AC ADL42875;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human ovarian cancer DNA marker #16765.

XX

KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX

OS Homo sapiens.

XX

PN WO200170979-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US009126.

XX

PR 21-MAR-2000; 2000US-0191031P.

XX

PR 25-MAY-2000; 2000US-0207124P.

XX

PR 15-JUN-2000; 2000US-0211940P.

XX

PR 07-JUL-2000; 2000US-0216820P.

XX

PR 25-JUL-2000; 2000US-0220661P.

XX

PR 21-DEC-2000; 2000US-0257672P.

XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

PI Lee J, Lillie J;

XX

DR WPI; 2001-611502/70.

XX

PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 PT cancer cells as compared to their normal non-cancerous ovarian cells are
 PT used to characterize stage, grade, histological type of ovarian cancer.

XX

PS Disclosure; SEQ ID NO 16765; 106pp; English.

XX

CC The invention relates to nucleic acid markers which are overexpressed in
 CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides
 CC encoded by the markers, antibodies that selectively bind to the
 CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
 CC of developing ovarian cancer involving inhibiting expression of a gene
 CC corresponding to a marker of the invention and a method of treating a
 CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a

CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 382 BP; 113 A; 69 C; 70 G; 130 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 382;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713

Db 101 TAAGTACCTCGCGCGACACGC 78
 |||||

RESULT 59

ADI76489/c

ID ADI76489 standard; DNA; 391 BP.

XX

AC ADI76489;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human ovarian cancer DNA marker #9231.

XX

KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX

OS Homo sapiens.

XX

PN WO200170979-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US009126.

XX

PR 21-MAR-2000; 2000US-0191031P.

XX

PR 25-MAY-2000; 2000US-0207124P.

XX

PR 15-JUN-2000; 2000US-0211940P.

XX

PR 07-JUL-2000; 2000US-0216820P.

XX

PR 25-JUL-2000; 2000US-0220661P.

XX

PR 21-DEC-2000; 2000US-0257672P.

XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

PI Lee J, Lillie J;

XX

DR WPI; 2001-611502/70.

XX

PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 PT cancer cells as compared to their normal non-cancerous ovarian cells are
 PT used to characterize stage, grade, histological type of ovarian cancer.
 XX Disclosure; SEQ ID NO 9231; 106pp; English.
 XX The invention relates to nucleic acid markers which are overexpressed in
 CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides
 CC encoded by the markers, antibodies that selectively bind to the
 CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
 CC of developing ovarian cancer involving inhibiting expression of a gene
 CC corresponding to a marker of the invention and a method of treating a
 CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a

CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 391 BP; 180 A; 42 C; 53 G; 116 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 60
AD170160/c
ID AD170160 standard; DNA; 391 BP.
XX
AC AD170160;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #2902.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
FR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
FA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
FI Lee J, Lillie J;
XX

DR WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
PS Disclosure; SEQ ID NO 2902; 106pp; English.

CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX Sequence 391 BP; 180 A; 42 C; 53 G; 116 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 61
ADL42485/c
ID ADL42485 standard; DNA; 391 BP.
XX
AC ADL42485;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #16375.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.

```
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-02116820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 16375; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 391 BP; 90 A; 74 C; 90 G; 137 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 391;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACTCTCGCGCGACACGC 1713
XX |||||||
XX Db 110 TAAGTACTCTCGCGCGACACGC 87
XX
XX RESULT 62
XX ADI76850/c
XX ID ADI76850 standard; DNA; 392 BP.
XX AC ADI76850;
XX CC
XX DT 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #9592.
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
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XX Homo sapiens.
XX OS
XX PN WO200170979-A2.
XX XX
XX PD 27-SEP-2001.
XX XX
XX PF 21-MAR-2001; 2001WO-US009126.
XX XX
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 9592; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX Query Match 1.4%; Score 24; DB 5; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACTCTCGCGCGACACGC 1713
XX |||||||
XX Db 30 TAAGTACTCTCGCGCGACACGC 7
XX
XX RESULT 63
XX ADI70525/c
```


RESULT 65
ADL42159/c
ID ADL42159 standard; DNA; 409 BP.
XX AC ADL42159;
XX DT 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #16049.
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX PS Disclosure; SEQ ID NO 16049; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 409 BP; 124 A; 85 C; 90 G; 110 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 5; Length 409;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGGACGACGC 1713
DB 111 TAAGTACTCTCGCGCGGACGACGC 88
RESULT 66
ADL43269/c
ID ADL43269 standard; DNA; 415 BP.
XX AC ADL43269;
XX DT 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #17159.
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX PS Disclosure; SEQ ID NO 17159; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The

CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 415 BP; 140 A; 73 C; 92 G; 110 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 415;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
Db 111 TAAGTACTCGCGCGACACGC 88

RESULT 67
ADL37618/c
ID ADL37618 standard; DNA; 416 BP.
XX
AC ADL37618;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #11508.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.

XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Lillie J;
XX
DR WPI; 2001-611502/70.

XX
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
PS Disclosure; SEQ ID NO 11508; 106pp; English.

XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the

CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX
SQ Sequence 416 BP; 128 A; 97 C; 62 G; 128 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 5; Length 416;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713
Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 68
ADI72479/c
ID ADI72479 standard; DNA; 416 BP.
XX
AC ADI72479;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #5221.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.

XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX
PI Lee J, Lillie J;
XX
DR WPI; 2001-611502/70.
XX
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
PS Disclosure; SEQ ID NO 5221; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides

CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 416 BP; 128 A; 97 C; 62 G; 128 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 5; Length 416;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTGGCGCGACCAAGC 1713
Db 30 TAAGTACTCTGGCGCGACCAAGC 7

RESULT 69

ADL38889
ID ADL38889 standard; DNA; 420 BP.

AC ADL38889;

DT 20-MAY-2004 (first entry)

DE Human ovarian cancer DNA marker #12779.

Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

OS Homo sapiens.

PN WO200170979-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US0009126.

PR 21-MAR-2000; 2000US-0191031P.

PR 25-MAY-2000; 2000US-0207124P.

PR 15-JUN-2000; 2000US-0211940P.

PR 07-JUL-2000; 2000US-0216820P.

PR 25-JUL-2000; 2000US-0220661P.

PR 21-DEC-2000; 2000US-0257672P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Lee J, Lillie J;

XX

DR WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.

PS Disclosure; SEQ ID NO 12779; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 420 BP; 126 A; 77 C; 77 G; 140 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTGGCGCGACCAAGC 1713

Db 391 TAAGTACTCTGGCGCGACCAAGC 414

RESULT 70

ADL41799/c

ID ADL41799 standard; DNA; 420 BP.

AC ADL41799;

DT 20-MAY-2004 (first entry)

DE Human ovarian cancer DNA marker #15689.

Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

OS Homo sapiens.

PN WO200170979-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US0009126.

XX

PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX
PI Lee J, Lillie J;
XX
DR WPI; 2001-611502/70.
XX
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX
PS Disclosure; SEQ ID NO 15689; 106pp; English.
XX
XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC expression levels indicates ovarian cancer sample. A difference between the
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 420 BP; 102 A; 83 C; 111 G; 124 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGACACGC 1713
DB 111 TAAGTACTCTCGCGCGACACGC 88
RESULT 71
AD173071
ID AD173071 standard; DNA; 421 BP.
XX
AC AD173071;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #5813.

XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
XX
PD 27-SEP-2001.
XX
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX
PI Lee J, Lillie J;
XX
DR WPI; 2001-611502/70.
XX
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX
PS Disclosure; SEQ ID NO 5813; 106pp; English.
XX
XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC expression levels indicates ovarian cancer sample. A difference between the
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 421 BP; 126 A; 77 C; 78 G; 140 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 5; Length 421;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTCGCGCGACACGC 1713
DB 391 TAAGTACTCTCGCGCGACACGC 414

RESULT 72
ABV39230/c
ID ABV39230 standard; cDNA; 424 BP.
XX
AC ABV39230;
XX
DT 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 39221.
XX
DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
OS
XX WO200160860-A2.
FN
XX 23-AUG-2001.
PD
XX
XX 20-FEB-2001; 2001WO-US005171.
PF
XX 17-FEB-2000; 2000US-0183319P.
PR
XX 16-MAR-2000; 2000US-0189862P.
PR
XX 25-MAY-2000; 2000US-0207454P.
PR
XX 09-JUN-2000; 2000US-0211314P.
PR
XX 18-JUL-2000; 2000US-0219007P.
PR
XX 13-DEC-2000; 2000US-0255281P.
PR
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Schlegel R, Endege WO, Monahan JE;
PI
XX WPI; 2001-662795/76.
DR
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 7963; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 424 BP; 120 A; 97 C; 88 G; 119 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 24; DB 5; Length 424;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 85 TAAGTACCTCGCGCGGACACGC 62
XX
RESULT 73
ACN86430/c
ID ACN86430 standard; DNA; 425 BP.
XX
AC ACN86430;
XX
DT 02-DEC-2004 (first entry)

XX Breast cancer related marker, seq id 7580.
DE
XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
KW
XX Homo sapiens.
OS
XX US2003099974-A1.
FN
XX 29-MAY-2003.
PD
XX 18-JUL-2002; 2002US-00198846.
PF
XX 18-JUL-2001; 2001US-0306220P.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI
XX WPI; 2003-787014/74.
DR
XX Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.
XX
XX Disclosure; SEQ ID NO 7580; 36pp; English.
XX
CC The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (SI). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?DocID=20030099974
XX
SQ Sequence 425 BP; 136 A; 92 C; 90 G; 106 T; 0 U; 1 Other;
XX
Query Match 1.4%; Score 24; DB 11; Length 425;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 105 TAAGTACCTCGCGCGGACACGC 82
XX
RESULT 74
ABV06575/c
ID ABV06575 standard; cDNA; 426 BP.
XX
XX AC ABV06575;
XX
XX 13-SEP-2002 (first entry)
DT
XX Human prostate expression marker cDNA 6566.
DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
OS
XX WO200160860-A2.
FN
XX 23-AUG-2001.
PD
XX 20-FEB-2001; 2001WO-US005171.
PF
XX 17-FEB-2000; 2000US-0183319P.
PR

```
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 1075; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 426 BP; 116 A; 102 C; 110 G; 98 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 426;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACCTCGCGCGACACGC 1713
XX |||||||||||||||||||
XX Db 30 TAAGTACCTCGCGCGACACGC 7
XX
XX RESULT 75
XX ADL44606/C
XX ID ADL44606 standard; DNA; 426 BP.
XX
XX AC ADL44606;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human ovarian cancer DNA marker #18496.
XX
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX OS Homo sapiens.
XX
XX PN WO200170979-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US009126.
XX
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 18496; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX
XX Sequence 426 BP; 176 A; 51 C; 47 G; 152 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 426;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1690 TAAGTACCTCGCGCGACACGC 1713
XX |||||||||||||||||||
XX Db 111 TAAGTACCTCGCGCGACACGC 88
XX
XX RESULT 76
XX ABV37925/C
XX ID ABV37925 standard; cDNA; 432 BP.
XX
XX AC ABV37925;
XX
XX DT 16-SEP-2002 (first entry)
XX
XX DE Human prostate expression marker cDNA 37916.
XX
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200160860-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 20-FEB-2001; 2001WO-US005171.
XX
XX PR 17-FEB-2000; 2000US-0183319P.
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PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 7755; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 432 BP; 153 A; 67 C; 75 G; 137 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 432;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1690 TAAGTACCTCGCGCGACCGC 1713
Db 56 TAAGTACCTCGCGCGACCGC 33
XX
RESULT 77
ADL44732/c
XX ADL44732 standard; DNA; 432 BP.
XX
XX ADL44732;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human ovarian cancer DNA marker #18622.
XX
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX Homo sapiens.
XX
XX WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US0009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX
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DR WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 18622; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX
XX Sequence 432 BP; 146 A; 93 C; 81 G; 112 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 5; Length 432;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1690 TAAGTACCTCGCGCGACCGC 1713
Db 95 TAAGTACCTCGCGCGACCGC 72
XX
RESULT 78
ADI70358/c
XX ADI70358 standard; DNA; 437 BP.
XX
XX AC ADI70358;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human ovarian cancer DNA marker #3100.
XX
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX Homo sapiens.
XX
XX WO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US0009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX
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PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
PI Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 3100; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX Sequence 437 BP; 102 A; 88 C; 91 G; 150 T; 0 U; 6 Other;

XX Query Match 1.4%; Score 24; DB 5; Length 437;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTCGCGCGACCAACGC 1713
Db |||||||
30 TAAGTACTCTCGCGCGACCAACGC 7

RESULT 79
ADI76684/c
ID ADI76684 standard; DNA; 437 BP.
XX
XX AC ADI76684;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human ovarian cancer DNA marker #9426.
XX
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX OS Homo sapiens.

XX WO200170979-A2.
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-0216820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 9426; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX Sequence 437 BP; 102 A; 88 C; 91 G; 150 T; 0 U; 6 Other;

XX Query Match 1.4%; Score 24; DB 5; Length 437;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCTCGCGCGACCAACGC 1713
Db |||||||
30 TAAGTACTCTCGCGCGACCAACGC 7

RESULT 80
ADL44126/c
ID ADL44126 standard; DNA; 442 BP.
XX

```
AC ADL44126;
XX 20-MAY-2004 (first entry)
XX Human ovarian cancer DNA marker #18016.
XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX Homo sapiens.
XX WO200170979-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009126.
XX 21-MAR-2000; 2000US-0191031P.
XX 25-MAY-2000; 2000US-0207124P.
XX 15-JUN-2000; 2000US-0211940P.
XX 07-JUL-2000; 2000US-02118820P.
XX 25-JUL-2000; 2000US-0220661P.
XX 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 18016; 106pp; English.
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX Sequence 442 BP; 116 A; 104 C; 111 G; 111 T; 0 U; 0 Other;
XX Query Match 1.4%; Score 24; DB 5; Length 442;
XX Best Local Similarity 100.0%; Pred. No. 1;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 444 BP; 152 A; 77 C; 116 G; 99 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 444;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 73 TAAGTACCTCGCGCGGACACGC 50

RESULT 82
ABV36041/c
ID ABV36041 standard; cDNA; 446 BP.

XX AC ABV36041;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 36032.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 7471; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (I) is useful for: (a) assessing whether
XX CC a patient is afflicted with prostate cancer; (b) monitoring the
XX CC progression of prostate cancer in a patient; (c) assessing the efficacy
XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX CC determining whether prostate cancer has metastasized in a patient; (h)
XX CC assessing the aggressiveness or indolence of prostate cancer in a patient
XX CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 446 BP; 137 A; 71 C; 85 G; 153 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 101 TAAGTACCTCGCGCGGACACGC 78

RESULT 83
ABV37972/c
ID ABV37972 standard; cDNA; 446 BP.

XX AC ABV37972;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 37963.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 7762; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (I) is useful for: (a) assessing whether
XX CC a patient is afflicted with prostate cancer; (b) monitoring the
XX CC progression of prostate cancer in a patient; (c) assessing the efficacy
XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX CC determining whether prostate cancer has metastasized in a patient; (h)
XX CC assessing the aggressiveness or indolence of prostate cancer in a patient
XX CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 446 BP; 139 A; 86 C; 56 G; 165 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 71 TAAGTACCTCGCGCGGACACGC 48

RESULT 84
ABV45101/c

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ID  ABV45101 standard; cDNA; 446 BP.
AC  ABV45101;
XX
XX  16-SEP-2002 (first entry)
XX
XX  Human prostate expression marker cDNA 45092.
XX
XX  Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW  pharmacogenomic marker; gene; ss.
XX
XX  Homo sapiens.
XX
XX  WO200150860-A2.
XX
XX  23-AUG-2001.
XX
XX  20-FEB-2001; 2001WO-US005171.
XX
XX  17-FEB-2000; 2000US-0183319P.
XX
XX  16-MAR-2000; 2000US-0189862P.
XX
XX  25-MAY-2000; 2000US-0207454P.
XX
XX  09-JUN-2000; 2000US-0211314P.
XX
XX  18-JUL-2000; 2000US-0219007P.
XX
XX  13-DEC-2000; 2000US-0255281P.
XX
XX  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX  Schlegel R, Endege WO, Monahan JE;
XX
XX  WPI; 2001-662795/76.
XX
XX  Novel isolated nucleic acid molecule associated with cancerous state of
PT  prostate cells and correlating with presence of prostate cancer, useful
PT  for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX  Claim 1; Page 8933; 11750pp; English.
XX
XX  The invention relates to an isolated nucleic acid molecule (I) comprising
CC  a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
CC  specification or its complement. (I) is useful for: (a) assessing whether
CC  a patient is afflicted with prostate cancer; (b) monitoring the
CC  progression of prostate cancer in a patient; (c) assessing the efficacy
CC  of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC  the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC  (e) selecting a composition for inhibiting prostate cancer in a patient;
CC  (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC  determining whether prostate cancer has metastasized in a patient; (h)
CC  assessing the aggressiveness or indolence of prostate cancer in a patient
CC  ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX  Sequence 446 BP; 137 A; 71 C; 85 G; 153 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 24; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 101 TAAGTACCTCGCGCGGACACGC 78
RESULT 85
ADL36720/c
ID ADL36720 standard; DNA; 446 BP.
XX
XX  ADL36720;
XX
XX  20-MAY-2004 (first entry)
XX
XX  Human ovarian cancer DNA marker #10610.
XX
XX  Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
XX  Homo sapiens.
XX
XX  WO200170979-A2.
XX
XX  27-SEP-2001.
XX
XX  21-MAR-2001; 2001WO-US009126.
XX
XX  21-MAR-2000; 2000US-0191031P.
XX
XX  25-MAY-2000; 2000US-0207124P.
XX
XX  15-JUN-2000; 2000US-0211940P.
XX
XX  07-JUL-2000; 2000US-0216820P.
XX
XX  25-JUL-2000; 2000US-0220661P.
XX
XX  21-DEC-2000; 2000US-0257672P.
XX
XX  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX  Lee J, Lillie J;
XX
XX  WPI; 2001-611502/70.
XX
XX  Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT  cancer cells as compared to their normal non-cancerous ovarian cells are
PT  used to characterize stage, grade, histological type of ovarian cancer.
XX
XX  Disclosure; SEQ ID NO 10610; 106pp; English.
XX
XX  The invention relates to nucleic acid markers which are overexpressed in
CC  ovarian cancer cells as compared to their expression in normal (i.e. non-
CC  cancerous) ovarian cells. The invention also relates to polypeptides
CC  encoded by the markers, antibodies that selectively bind to the
CC  polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC  of developing ovarian cancer involving inhibiting expression of a gene
CC  corresponding to a marker of the invention and a method of treating a
CC  patient afflicted with ovarian cancer comprising providing to cells of
CC  the patient an antisense oligonucleotide complementary to a marker of the
CC  invention. The markers are useful for assessing if a patient is afflicted
CC  with ovarian cancer, which involves comparing the level of expression of
CC  a marker in a patient sample and a normal level of expression of the
CC  marker in a control non-ovarian cancer sample. A difference between the
CC  expression levels indicates ovarian cancer. The level of expression of a
CC  marker corresponds to a secreted protein or to a transcribed
CC  polynucleotide or its portion. The level of expression of the marker is
CC  assessed by detecting the presence in the sample, a protein or protein
CC  fragment corresponding to the marker. The presence of protein or protein
CC  fragment is detected using an antibody that specifically binds with the
CC  protein or protein fragment. Alternatively, the level of expression of
CC  the marker is assessed by detecting the presence of a transcribed
CC  polynucleotide which anneals with the marker or anneals with a portion of
CC  the polynucleotide comprising the marker, under stringent conditions. The
CC  marker is also used for monitoring the progression of ovarian cancer in a
CC  patient which involves detecting expression of the marker in a patient
CC  sample at a first point in time, repeating the method at a subsequent
CC  time and comparing the level of expression. The method is carried out
CC  using an ovarian tissue sample. A composition comprising a marker,
CC  polypeptide or antibody of the invention is used to treat ovarian cancer.
CC  This sequence represents a human ovarian cancer DNA marker of the
CC  invention.
XX
XX  Sequence 446 BP; 123 A; 114 C; 85 G; 123 T; 0 U; 1 Other;
SQ
Query Match 1.4%; Score 24; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 30 TAAGTACCTCGCGCGGACACGC 7
RESULT 86
ADI71564/c
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PR 05-SEP-2000; 2000US-0229509P.
PR 06-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
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PR 02-OCT-2000; 2000US-0236802P.
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PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
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PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246533P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
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PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.

PR 17-NOV-2000; 2000US-0249216P.
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PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
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PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-541565/60.
XX P-PSDB; ABB14802.
DR
DR Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system cancers
PT and metastases.
XX
PS Claim 1; SEQ ID NO 135; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 449 BP; 106 A; 99 C; 102 G; 141 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 5; Length 449;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
|||||
Db 56 TAAGTACCTCGCGCGGACACGC 33

RESULT 88
ABQ75327/c
ID ABQ75327 standard; cDNA; 457 BP.
XX
XX AC ABQ75327;
XX
XX DT 05-NOV-2002 (first entry)

XX DE Human lung specific nucleic acid sequence SEQ ID NO:66.
XX KW Human; lung; lung specific nucleic acid; LSNA; lung specific protein;
XX LW LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer;
XX KW squamous cell carcinoma; gene; chromosome 8; ss.
XX OS Homo sapiens.
XX XX WO200264788-A2.
XX PN 22-AUG-2002.
XX PD 20-NOV-2001; 2001WO-US045080.
XX PF 20-NOV-2000; 2000US-0252054P.
XX PR (DIAD-) DIADEXUS INC.
XX PA Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX PI WPI; 2002-657601/70.
XX DR New lung specific nucleic acid useful in gene therapy or as vaccines for
XX PT treating lung cancer (e.g. squamous cell carcinoma) or non-cancerous lung
XX PT diseases, as well as for diagnosing, monitoring or staging these
XX PT diseases.
XX PS Claim 1; Page 186; 282pp; English.
XX XX The present invention describes an isolated lung specific nucleic acid
XX CC (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid
XX CC sequences comprising 17 - 733 amino acids, given in ABP52873 to ABP52965;
XX CC (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp),
XX CC given in ABQ75262 to ABQ75376; (c) selectively hybridizes to (a) or (b);
XX CC or (d) has 60 % sequence identity to (a) or (b). LSNA and lung specific
XX CC protein (LSP) sequences have cytostatic activity and can be used in gene
XX CC therapy and vaccines. LSNA and LSPs are useful for diagnosing and
XX CC monitoring the presence and metastases of lung cancer in a patient. An
XX CC antibody that specifically binds to an LSP can be used for determining
XX CC the presence of an LSP in a sample, as well as for treating a patient
XX CC with lung cancer, particularly by inducing an immune response against the
XX CC lung cancer cell expressing the LSNA or LSPs. In particular, these LSNA
XX CC and LSPs are useful for identifying, diagnosing, monitoring, staging,
XX CC imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-
XX CC cancerous disease states in lung
XX SQ Sequence 457 BP; 163 A; 70 C; 100 G; 124 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 6; Length 457;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1690 TAAGTACTCTCGCGCGACCAACGC 1713
Db 24 TAAGTACTCTCGCGCGACCAACGC 1
|||||
RESULT 89
ADL44815/c
ID ADL44815 standard; DNA; 460 BP.
XX AC ADL44815;
XX XX 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #18705.
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX XX WO200170979-A2.
XX PN

XX PD 27-SEP-2001.
XX XX 21-MAR-2001; 2001WO-US009126.
XX PF 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lee J, Lillie J;
XX XX WPI; 2001-611502/70.
XX DR Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX PT cancer cells as compared to their normal non-cancerous ovarian cells are
XX PT used to characterize stage, grade, histological type of ovarian cancer.
XX PS Disclosure; SEQ ID NO 18705; 106pp; English.
XX XX The invention relates to nucleic acid markers which are overexpressed in
XX CC ovarian cancer cells as compared to their expression in normal (i.e. non-
XX CC cancerous) ovarian cells. The invention also relates to polypeptides
XX CC encoded by the markers, antibodies that selectively bind to the
XX CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX CC of developing ovarian cancer involving inhibiting expression of a gene
XX CC corresponding to a marker of the invention and a method of treating a
XX CC patient afflicted with ovarian cancer comprising providing to cells of the
XX CC invention an antisense oligonucleotide complementary to a marker of the
XX CC invention. The markers are useful for assessing if a patient is afflicted
XX CC with ovarian cancer, which involves comparing the level of expression of
XX CC a marker in a patient sample and a normal level of expression of the
XX CC marker in a control non-ovarian cancer sample. A difference between the
XX CC expression levels indicates ovarian cancer. The level of expression of a
XX CC marker corresponds to a secreted protein or to a transcribed
XX CC polynucleotide or its portion. The level of expression of the marker is
XX CC assessed by detecting the presence in the sample, a protein or protein
XX CC fragment corresponding to the marker. The presence of protein or protein
XX CC fragment is detected using an antibody that specifically binds with the
XX CC protein or protein fragment. Alternatively, the level of expression of
XX CC the marker is assessed by detecting the presence of a transcribed
XX CC polynucleotide which anneals with the marker or anneals with a portion of
XX CC the polynucleotide comprising the marker, under stringent conditions. The
XX CC marker is also used for monitoring the progression of ovarian cancer in a
XX CC patient which involves detecting expression of the marker in a patient
XX CC sample at a first point in time, repeating the method at a subsequent
XX CC time and comparing the level of expression. The method is carried out
XX CC using an ovarian tissue sample. A composition comprising a marker,
XX CC polypeptide or antibody of the invention is used to treat ovarian cancer.
XX CC This sequence represents a human ovarian cancer DNA marker of the
XX CC invention. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 460 BP; 92 A; 98 C; 103 G; 167 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 5; Length 460;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1690 TAAGTACTCTCGCGCGACCAACGC 1713
Db 108 TAAGTACTCTCGCGCGACCAACGC 85
|||||
RESULT 90
ACN84351/c
ID ACN84351 standard; DNA; 463 BP.
XX XX

KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 9665; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 464 BP; 146 A; 91 C; 92 G; 116 T; 0 U; 19 Other;

Query Match 1.4%; Score 24; DB 5; Length 464;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 93

ADL41961/c

ID ADL41961 standard; DNA; 471 BP.

XX ADL41961;

XX 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #15851.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 15851; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 471 BP; 132 A; 68 C; 104 G; 167 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 5; Length 471;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTGGCGCGGACACGC 1713
|||||
Db 103 TAAGTACTCTGGCGCGGACACGC 80
|||||
RESULT 94
ADL36885/c
ID ADL36885 standard; DNA; 486 BP.
XX AC ADL36885;
XX DT 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #10775.
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX DR Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX PT cancer cells as compared to their normal non-cancerous ovarian cells are
XX PT used to characterize stage, grade, histological type of ovarian cancer.
XX PS Disclosure; SEQ ID NO 10775; 106pp; English.
XX CC The invention relates to nucleic acid markers which are overexpressed in
XX CC ovarian cancer cells as compared to their expression in normal (i.e. non-
XX CC cancerous) ovarian cells. The invention also relates to polypeptides
XX CC encoded by the markers, antibodies that selectively bind to the
XX CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX CC of developing ovarian cancer involving inhibiting expression of a gene
XX CC corresponding to a marker of the invention and a method of treating a
XX CC patient afflicted with ovarian cancer comprising providing to cells of
XX CC the patient an antisense oligonucleotide complementary to a marker of the
XX CC invention. The markers are useful for assessing if a patient is afflicted
XX CC with ovarian cancer, which involves comparing the level of expression of
XX CC a marker in a patient sample and a normal level of expression of the
XX CC marker in a control non-ovarian cancer sample. A difference between the
XX CC expression levels indicates ovarian cancer. The level of expression of a
XX CC marker corresponds to a secreted protein or to a transcribed
XX CC polynucleotide or its portion. The level of expression of the marker is
XX CC assessed by detecting the presence in the sample, a protein or protein
XX CC fragment corresponding to the marker. The presence of protein or protein
XX CC fragment is detected using an antibody that specifically binds with the
XX CC protein or protein fragment. Alternatively, the level of expression of
XX CC the marker is assessed by detecting the presence of a transcribed
XX CC polynucleotide which anneals with the marker or anneals with a portion of

CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker, cancer,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 486 BP; 177 A; 69 C; 86 G; 135 T; 0 U; 19 Other;
Query Match 1.4%; Score 24; DB 5; Length 486;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACTCTGGCGCGGACACGC 1713
|||||
Db 30 TAAGTACTCTGGCGCGGACACGC 7
|||||
RESULT 95
ADI71730/c
ID ADI71730 standard; DNA; 486 BP.
XX AC ADI71730;
XX DT 20-MAY-2004 (first entry)
XX DE Human ovarian cancer DNA marker #4472.
XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX OS Homo sapiens.
XX PN WO200170979-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009126.
XX PR 21-MAR-2000; 2000US-0191031P.
XX PR 25-MAY-2000; 2000US-0207124P.
XX PR 15-JUN-2000; 2000US-0211940P.
XX PR 07-JUL-2000; 2000US-0216820P.
XX PR 25-JUL-2000; 2000US-0220661P.
XX PR 21-DEC-2000; 2000US-0257672P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX DR Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX PT cancer cells as compared to their normal non-cancerous ovarian cells are
XX PT used to characterize stage, grade, histological type of ovarian cancer.
XX PS Disclosure; SEQ ID NO 4472; 106pp; English.
XX CC The invention relates to nucleic acid markers which are overexpressed in
XX CC ovarian cancer cells as compared to their expression in normal (i.e. non-
XX CC cancerous) ovarian cells. The invention also relates to polypeptides
XX CC encoded by the markers, antibodies that selectively bind to the
XX CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX CC of developing ovarian cancer involving inhibiting expression of a gene
XX CC corresponding to a marker of the invention and a method of treating a
XX CC patient afflicted with ovarian cancer comprising providing to cells of
XX CC the patient an antisense oligonucleotide complementary to a marker of the
XX CC invention. The markers are useful for assessing if a patient is afflicted
XX CC with ovarian cancer, which involves comparing the level of expression of

CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX SQ Sequence 486 BP; 177 A; 69 C; 86 G; 135 T; 0 U; 19 Other;
Query Match 1.4%; Score 24; DB 5; Length 486;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAACTACTCTGGCGCGACACGCG 1713
Db 30 TAACTACTCTGGCGCGACACGCG 7
|||||

RESULT 96

AAH69562/C

ID AAH69562 standard; cDNA; 500 BP.

XX AC AAH69562;

XX DT 19-SEP-2001 (first entry)

XX DE Human cervical cancer marker nucleic acid 836.

XX KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

XX OS Homo sapiens.

XX FN WO200142467-A2.

XX FD 14-JUN-2001.

XX PF 08-DEC-2000; 2000WO-US033312.

XX PR 08-DEC-1999; 99US-0169681P.

XX PR 21-DEC-1999; 99US-0171350P.

XX PR 14-MAR-2000; 2000US-0189315P.

XX PR 12-MAY-2000; 2000US-0203791P.

XX PR 09-JUN-2000; 2000US-0210600P.

XX PR 21-JUL-2000; 2000US-0220114P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Deeds J, Berger A, Zhao X;

XX DR WPI; 2001-375006/39.

XX PT New isolated nucleic acid for diagnosing and treating cervical cancer and
XX PT for assessing and detecting compounds for treating the cancer.

XX PS Claim 1; Page 244-245; 1051pp; English.

XX CC The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with

CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy

XX SQ Sequence 500 BP; 145 A; 108 C; 99 G; 148 T; 0 U; 0 Other;
Query Match 1.4%; Score 24; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAACTACTCTGGCGCGACACGCG 1713

Db 30 TAACTACTCTGGCGCGACACGCG 7
|||||

RESULT 97

ADL42477/C

ID ADL42477 standard; DNA; 503 BP.

XX AC ADL42477;

XX DT 20-MAY-2004 (first entry)

XX DE Human ovarian cancer DNA marker #16367.

XX KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX OS Homo sapiens.

XX FN WO200170979-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009126.

XX PR 21-MAR-2000; 2000US-0191031P.

XX PR 25-MAY-2000; 2000US-0207124P.

XX PR 15-JUN-2000; 2000US-0211940P.

XX PR 07-JUL-2000; 2000US-0216820P.

XX PR 25-JUL-2000; 2000US-0220661P.

XX PR 21-DEC-2000; 2000US-0257672P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lee J, Illie J;

XX DR WPI; 2001-611502/70.

XX PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX PT cancer cells as compared to their normal non-cancerous ovarian cells are
XX PT used to characterize stage, grade, histological type of ovarian cancer.

XX PS Disclosure; SEQ ID NO 16367; 106pp; English.

XX CC The invention relates to nucleic acid markers which are overexpressed in
XX CC ovarian cancer cells as compared to their expression in normal (i.e. non-
XX CC cancerous) ovarian cells. The invention also relates to polypeptides
XX CC encoded by the markers, antibodies that selectively bind to the
XX CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX CC of developing ovarian cancer involving inhibiting expression of a gene
XX CC corresponding to a marker of the invention and a method of treating a
XX CC patient afflicted with ovarian cancer comprising providing to cells of
XX CC the patient an antisense oligonucleotide complementary to a marker of the
XX CC invention. The markers are useful for assessing if a patient is afflicted
XX CC with ovarian cancer, which involves comparing the level of expression of
XX CC a marker in a patient sample and a normal level of expression of the
XX CC marker in a control non-ovarian cancer sample. A difference between the
XX CC expression levels indicates ovarian cancer. The level of expression of a
XX CC marker corresponds to a secreted protein or to a transcribed
XX CC polynucleotide or its portion. The level of expression of the marker is
XX CC assessed by detecting the presence in the sample, a protein or protein

CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 503 BP; 166 A; 92 C; 74 G; 170 T; 0 U; 1 Other;

Query Match 1.4%; Score 24; DB 5; Length 503;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAACTACCTCGCGCGGACCGC 1713

DB 85 TAACTACCTCGCGCGGACCGC 62

RESULT 98

ADL42086/c

ID ADL42086 standard; DNA; 517 BP.

XX AC

XX ADL42086;

XX 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #15976.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 15976; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene

CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.

XX SQ Sequence 517 BP; 145 A; 76 C; 111 G; 185 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 517;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAACTACCTCGCGCGGACCGC 1713

DB 102 TAACTACCTCGCGCGGACCGC 79

RESULT 99

AD172251/c

ID AD172251 standard; DNA; 521 BP.

XX AC

XX AD172251;

XX 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #4993.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

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XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 4993; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in

XX ovarian cancer cells as compared to their expression in normal (i.e. non-

XX cancerous) ovarian cells. The invention also relates to polypeptides

XX encoded by the markers, antibodies that selectively bind to the

XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk

XX of developing ovarian cancer involving inhibiting expression of a gene

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XX the polynucleotide comprising the marker, under stringent conditions. The

XX marker is also used for monitoring the progression of ovarian cancer in a

XX patient which involves detecting expression of the marker in a patient

XX sample at a first point in time, repeating the method at a subsequent

XX time and comparing the level of expression. The method is carried out

XX using an ovarian tissue sample. A composition comprising a marker,

XX polypeptide or antibody of the invention is used to treat ovarian cancer.

XX This sequence represents a human ovarian cancer DNA marker of the

XX invention. Note: The sequence data for this patent did not form part of

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 521 BP; 110 A; 132 C; 124 G; 153 T; 0 U; 2 Other;

Query Match 1.4%; Score 24; DB 5; Length 521;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 30 TAAGTACTCGCGCGACACGC 7

RESULT 100

ADL41725/C

ID ADL41725 standard; DNA; 521 BP.

XX AC ADL41725;

XX 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #15615.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

PR 21-DEC-2000; 2000US-0257672P.

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XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

XX cancer cells as compared to their normal non-cancerous ovarian cells are

XX used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 15615; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in

XX ovarian cancer cells as compared to their expression in normal (i.e. non-

XX cancerous) ovarian cells. The invention also relates to polypeptides

XX encoded by the markers, antibodies that selectively bind to the

XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk

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XX invention. Note: The sequence data for this patent did not form part of

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 521 BP; 214 A; 69 C; 88 G; 150 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 5; Length 521;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 TAAGTACTCGCGCGACACGC 1713

Db 106 TAAGTACTCGCGCGACACGC 83

Search completed: March 11, 2006, 20:34:15

Job time : 1079 secs

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 20:16:33 ; Search time 6306 Seconds
(without alignments)
12709.526 Million cell updates/sec

Title: US-09-989-890-105

Perfect score: 1713

Sequence: 1 agccccgcctggacaccc.....tacctggcgagaccacgc 1713

Scoring-table: OLIGO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word-size: 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hic:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1361	79.5	1671	4	CR749558
2	1197	69.9	1197	11	DQ045548 Homo sapi
3	752	43.9	975	3	BM460277 AGENCOURT
4	635	37.1	917	5	BQ691555 AGENCOURT
5	622	36.3	622	3	BM823479 K-EST0094
6	598	34.9	753	7	CN289134 170005999
7	528	30.8	582	3	BP315176 BP315176
8	510	29.8	510	1	AA316608 EST188290
9	491	28.7	1181	11	DQ045549
10	480	28.0	489	1	AI925416
11	450	26.3	470	5	BE110746
12	450	26.3	966	2	BE901537
13	424	24.8	583	3	BP315124
14	370	21.6	370	1	AW589267
15	323	18.9	513	6	CD702656
16	303	18.7	330	1	AI702452
17	321	17.7	1015	2	BE741035
18	291	17.0	556	1	AA573775
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20	215	12.6	423	1	AW008047
21	213	12.4	244	2	BE162756
22	208	12.1	246	3	BM750392

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101	26	1.5	746	3	BI905189	603167516	C 174	24	1.4	174	8	CV971679	CV971679	LRRG0167
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146	25	1.5	655	7	CO498240	G.h.fbr-s	C 219	24	1.4	219	6	CA737687	CA737687	wpi2s.pk0
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163	24	1.4	151	6	CF048886	QCL28g08	C 236	24	1.4	236	6	CA737687	CA737687	wpi2s.pk0
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C 244	24	1.4	248	8	CV971863	CV971863 LRRGE0186	C 317	24	1.4	314	6	CF061027	CF061027 QCN165008
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C 246	24	1.4	250	8	CV971789	CV971789 LRRGE0178	C 319	24	1.4	318	6	CB708394	CB708394 AMGNNUC:S
C 247	24	1.4	250	8	CV972906	CV972906 LRRGE0290	C 320	24	1.4	318	6	CF048958	CF048958 QCN29005
C 248	24	1.4	251	6	CD987982	CD987982 LRRGE0237	C 321	24	1.4	318	6	CF053993	CF053993 QCN23602
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C 253	24	1.4	256	8	CV972340	CV972340 LRRGE0234	C 326	24	1.4	326	1	AL729207	AL729207 AL729207
C 254	24	1.4	256	8	CV972385	CV972385 LRRGE0238	C 327	24	1.4	327	1	AJ746818	AJ746818 AJ746818
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C 256	24	1.4	259	6	CF062729	CF062729 QCN12h10	C 329	24	1.4	330	8	CV972998	CV972998 LRRGE0299
C 257	24	1.4	259	8	CV972010	CV972010 LRRGE0201	C 330	24	1.4	331	1	AW682514	AW682514 EST01363
C 258	24	1.4	263	8	CV971625	CV971625 LRRGE0162	C 331	24	1.4	332	8	CV972936	CV972936 LRRGE0293
C 259	24	1.4	268	8	CV971941	CV971941 LRRGE0194	C 332	24	1.4	333	8	CV888589	CV888589 LRRGE0048
C 260	24	1.4	269	6	CA745301	CA745301 wr118.pk0	C 333	24	1.4	336	6	CA736806	CA736806 wr118.pk0
C 261	24	1.4	270	1	AL718701	AL718701	C 334	24	1.4	337	6	CF800490	CF800490 EST00011.M
C 262	24	1.4	270	6	CF053980	CF053980 QCN23C10	C 335	24	1.4	337	6	CF800550	CF800550 EST00071.M
C 263	24	1.4	270	6	CF054088	CF054088 QCN24G10	C 336	24	1.4	340	6	CB694231	CB694231 AMGNNUC:S
C 264	24	1.4	270	6	CF054150	CF054150 QCN25607	C 337	24	1.4	341	6	CB693915	CB693915 AMGNNUC:S
C 265	24	1.4	270	6	CF054174	CF054174 QCN25610	C 338	24	1.4	341	8	CV888459	CV888459 LRRGE0035
C 266	24	1.4	270	6	CF054270	CF054270 QCN27D12	C 339	24	1.4	341	8	CV888866	CV888866 LRRGE0075
C 267	24	1.4	270	6	CF054429	CF054429 QCN29C08	C 340	24	1.4	343	1	AL727759	AL727759 AL727759
C 268	24	1.4	270	6	CF054694	CF054694 QCN31906	C 341	24	1.4	344	8	CV972098	CV972098 LRRGE0209
C 269	24	1.4	270	8	CV971702	CV971702 LRRGE0170	C 342	24	1.4	346	8	CV888613	CV888613 LRRGE0050
C 270	24	1.4	273	8	CV888789	CV888789 LRRGE0068	C 343	24	1.4	346	8	CV888754	CV888754 LRRGE0064
C 271	24	1.4	276	6	CA743006	CA743006 wr118.pk0	C 344	24	1.4	353	6	CA736644	CA736644 wr118.pk0
C 272	24	1.4	276	6	CF053969	CF053969 QCN23B05	C 345	24	1.4	353	6	DN976310	DN976310 Gp_mabB0
C 273	24	1.4	277	6	CF051228	CF051228 QCN22H08	C 346	24	1.4	354	6	CA736245	CA736245 wr118.pk0
C 274	24	1.4	277	7	CN121113	CN121113 EST122-C0	C 347	24	1.4	354	6	CA736685	CA736685 wr118.pk0
C 275	24	1.4	280	6	CA735250	CA735250 wr118.pk0	C 348	24	1.4	355	6	CA736939	CA736939 wr118.pk0
C 276	24	1.4	282	5	BQ580373	BQ580373 EST-SF-00	C 349	24	1.4	357	7	CO499783	CO499783 G.h.fbr-s
C 277	24	1.4	282	6	CA735019	CA735019 wr118.pk0	C 350	24	1.4	357	8	CO568105	CO568105 1322922.N
C 278	24	1.4	284	8	CV972179	CV972179 LRRGE0217	C 351	24	1.4	358	8	CV972089	CV972089 LRRGE0208
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C 281	24	1.4	286	6	CB711104	CB711104 AMGNNUC:S	C 354	24	1.4	360	6	CA736173	CA736173 wr118.pk0
C 282	24	1.4	287	1	AL723262	AL723262	C 355	24	1.4	360	6	CA744861	CA744861 wr118.pk0
C 283	24	1.4	287	7	CO494502	CO494502 G.h.fbr-s	C 356	24	1.4	360	7	CV186322	CV186322 Lr.RS1CF
C 284	24	1.4	288	6	CF054710	CF054710 QCN31h12	C 357	24	1.4	361	8	DN911004	DN911004 C745.Supp
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C 286	24	1.4	289	1	AA933277	AA933277 SWBmL3SA4	C 359	24	1.4	363	6	CA735367	CA735367 wr118.pk0
C 287	24	1.4	289	1	AL726365	AL726365	C 360	24	1.4	363	6	CA735376	CA735376 wr118.pk0
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C 289	24	1.4	289	7	CO491636	CO491636 G.h.fbr-s	C 362	24	1.4	363	8	CV973006	CV973006 LRRGE0300
C 290	24	1.4	292	6	CF054920	CF054920 QCN34F11	C 363	24	1.4	366	6	CA735476	CA735476 wr118.pk0
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C 294	24	1.4	294	8	CO566675	CO566675 1320936.N	C 367	24	1.4	370	6	CD051308	CD051308 EST0657.S
C 295	24	1.4	296	6	CF061287	CF061287 QCN19h05	C 368	24	1.4	371	8	CV972607	CV972607 LRRGE0260
C 296	24	1.4	300	1	AW681436	AW681436 EST00154	C 369	24	1.4	373	1	AL726483	AL726483 AL726483
C 297	24	1.4	300	8	CV972382	CV972382 LRRGE0238	C 370	24	1.4	375	1	AI079069	AI079069 SWBmL3SBH
C 298	24	1.4	301	8	CV972665	CV972665 LRRGE0266	C 371	24	1.4	376	6	CA735131	CA735131 wr118.pk0
C 299	24	1.4	302	1	AL722343	AL722343	C 372	24	1.4	377	1	AW682168	AW682168 EST00935
C 300	24	1.4	302	1	AW681908	AW681908 EST00626	C 373	24	1.4	381	1	AL717711	AL717711
C 301	24	1.4	303	1	AW681753	AW681753 EST00471	C 374	24	1.4	381	6	CF059676	CF059676 QCN515C11
C 302	24	1.4	303	8	CX125995	gamEST.80	C 375	24	1.4	381	6	CF569158	CF569158 EST019.Su
C 303	24	1.4	304	7	CO497484	CO497484 G.h.fbr-s	C 376	24	1.4	382	8	CV888255	CV888255 LRRGE0014
C 304	24	1.4	304	8	CX943962	CX943962 DH0AGB122	C 377	24	1.4	382	8	CV888437	CV888437 LRRGE0032
C 305	24	1.4	306	7	CK928056	CK928056 haap006xk	C 378	24	1.4	384	7	CV700372	CV700372 PJS-08-H0
C 306	24	1.4	306	8	CV972623	CV972623 LRRGE0262	C 379	24	1.4	385	1	AJ568378	AJ568378
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C 308	24	1.4	310	6	CB697136	CB697136 AMGNNUC:S	C 381	24	1.4	387	7	CF922789	CF922789 gmrhww24
C 309	24	1.4	310	8	CV972856	CV972856 LRRGE0285	C 382	24	1.4	387	7	CV700192	CV700192 PJS-06-E0
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C 311	24	1.4	311	6	CB696756	CB696756 AMGNNUC:S	C 384	24	1.4	390	8	CV972915	CV972915 LRRGE0291
C 312	24	1.4	311	7	CO494812	CO494812 G.h.fbr-s	C 385	24	1.4	392	6	CA746361	CA746361 wr128.pk0
C 313	24	1.4	311	7	CO495865	CO495865 G.h.fbr-s	C 386	24	1.4	393	7	CO497659	CO497659 G.h.fbr-s
C 314	24	1.4	312	7	CO493506	CO493506 G.h.fbr-s	C 387	24	1.4	393	8	CV972911	CV972911 LRRGE0291

C 388	24	1.4	394	8	CV888266	CV888266	LRRG0015	C 461	24	1.4	510	1	AL725812	AL725812
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C 397	24	1.4	408	6	CB770406	ANGNUC:S	CB770406	C 470	24	1.4	523	6	CA743604	CA743604
C 398	24	1.4	409	6	CF036166	QCG28d11	CF036166	C 471	24	1.4	523	6	CA743950	CA743950
C 399	24	1.4	414	7	CN072146	B327_Pax1	CN072146	C 472	24	1.4	523	6	CF060507	QCT10c09
C 400	24	1.4	417	6	CF049280	QCL33e08	CF049280	C 473	24	1.4	524	6	CF055192	QCN38c02
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C 402	24	1.4	418	6	CD975066	QAE53a07	CD975066	C 475	24	1.4	526	6	CF060513	QCT10d03
C 403	24	1.4	419	6	CB764922	ANGNUC:N	CB764922	C 476	24	1.4	536	1	AW682236	EST01018
C 404	24	1.4	421	6	CB764383	ANGNUC:S	CB764383	C 477	24	1.4	537	6	CF057554	CF057554
C 405	24	1.4	423	6	CA738150	WP128.pk0	CA738150	C 478	24	1.4	542	1	AL719579	AL719579
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C 407	24	1.4	427	6	CA736482	WP11s.pk0	CA736482	C 480	24	1.4	542	7	CV699731	CV699731
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C 414	24	1.4	437	1	AL717820	AL717820	AL717820	C 487	24	1.4	557	1	AL722414	AL722414
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C 416	24	1.4	441	6	CF049035	QCL30a03	CF049035	C 489	24	1.4	558	1	AL724218	AL724218
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C 419	24	1.4	446	8	CO494138	DH0AGB15Z	CO494138	C 492	24	1.4	559	6	CF039272	CF039272
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ALIGNMENTS

RESULT 1

CR749558	CR749558	1671 bp	mRNA	linear	HTC	19-AUG-2004
LOCUS	Homo sapiens mRNA; cDNA DKFZp686B17277 (from clone DKFZp686B17277).					
DEFINITION						
ACCESSION	CR749558					
VERSION	CR749558.1	GI:51476784				
KEYWORDS	HTC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
	Hominidae; Homo.					
REFERENCE	1 (bases 1 to 1671)					
AUTHORS	Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,					
	Newes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and					
	Wiemann,S.					
CONSTRM	The German cDNA Consortium					
TITLE	Direct Submission					
JOURNAL	Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764					
	Neuberberg, GERMANY					
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer					
	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;					
	sequenced by DKFZ (German Cancer Research Center,					
	Heidelberg/Germany) within the cDNA sequencing consortium of the					
	German Genome Project. This clone (DKFZp686B17277) is available at					
	the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in					
	Berlin, Germany. Please contact RZPD for ordering:					
	http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp686B17277					

Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

FEATURES
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ORIGIN

Query Match 79.5%; Score 1361; DB 4; Length 1671;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 286 CTTGCTCTACTAGGACTCCACTGAGGGGACTGTGGAAGCAACTGGGCCAAGAGGACAA 345
QY 396 TGGAGTCCCCCAGCCCTCATCTGTGACACCCCGGCGGATGGCCAGCGGCTCAA 455
DB 346 TGGAGTCCCCCAGCCCTCATCTGTGACACCCCGGCGGATGGCCAGCGGCTCAA 405
QY 456 GTCAACCATGGGACGACTTCAGCTACCCCGATGTTAAGCTCAAGGCGATCCCTGTGTA 515
DB 406 GTCAACCATGGGACGACTTCAGCTACCCCGATGTTAAGCTCAAGGCGATCCCTGTGTA 465
QY 516 TCCTTACCCGAGGACACTCCCGAGCCCTGTGAGGAGCTCTCTGTGCAAGGAGCCACT 575
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QY 936 CCACAGACCTCGAGGGTCTGTTCAACTCGGGTCTGCCCCAACCGCTGCTGCCCTGA 995

DB 886 CCACAGACCTCGAGGGTCTGTTCAACTCGGGCTGTGCCCCAACCCGCTGCTGCCCTGA 945
QY 996 CAGTGGCCATGAGACCATGCTGGGCTCAGCTCTCAGCCAGGATGAGCTGACAGTGCAGAT 1055
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DB 1126 CTTGCTCCAGGTGTACTGCTTAAACCCCTGCCAGGCCACAGCTGCCACACCCCTTTCTGGGAGA 1185
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DB 1186 AGCATGGCCTACAGATGAGAGGGGACAGGACACCCCTGTGGGAGAGGCTTAGACCTG 1245
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DB 1366 GCCCTTCTCTCTGCTCATGCTTTCAGTGGCTTTCAGTGGCTGATCATGGAAGATGAGGATTTAGG 1425
QY 1476 CATTACCTCTGGGAGTGAACTGACTCCATCCCTTATGTCACCCCTTAAACCAATCATG 1535
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QY 1596 TATTGGGGGTGGGAGGCGCCACTCTATGTTATGTTAAGAGTGGTCTTCTGTTCTGG 1655
DB 1546 TATTGGGGGTGGGAGGCGCCACTCTATGTTATGTTAAGAGTGGTCTTCTGTTCTGG 1605
QY 1656 CTGATGTTCTGATCTTAAACATGACACAGCTTTGTAAGTAC 1696
DB 1606 CTGATGTTCTGATCTTAAACATGACACAGCTTTGTAAGTAC 1646

RESULT 2
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LOCUS DQ045548 1197 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens FLJ34633 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ045548
VERSION DQ045548.1 GI:66896763
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1197)
AUTHORS Nielsen,R., Bustanante,C., Clark,A.G., Gnanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
KEYWORDS 2 (bases 1 to 1197)
REFERENCE

AUTHORS Nieleen, R., Bustamante, C., Clark, A. G., Gianowski, S., Sackton, T. B.,
Hubisz, M. J., Fiedel-Alon, A., Tanenbaum, D. M., Civello, D.,
White, T. J., Skinsky, J. J., Adams, M. D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
gene <1..>1197
/gene="FLJ34633"
/locus_tag="HC11301"

ORIGIN
Query Match 59.9%; Score 1197; DB 11; Length 1197;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCGCCCTGGACACCCGCCCCAGCATCTGGGCTCCACGCTTGGAGCCGTGGAG 60
DB 1 ATGCCCGCCCTGGACACCCGCCCCAGCATCTGGGCTCCACGCTTGGAGCCGTGGAG 60
QY 61 CGGCCAACAGAGATATGTCTGGAGACATATGATAAACACCTCAGCCCCCACAAGCCGC 120
DB 61 CGGCCAACAGAGATATGTCTGGAGACATATGATAAACACCTCAGCCCCCACAAGCCGC 120
QY 121 CGCACCGCTAGACAGACCCCAAGGACCCTGGCCACATGGGCCAGAGCATTACTTTC 180
DB 121 CGCACCGCTAGACAGACCCCAAGGACCCTGGCCACATGGGCCAGAGCATTACTTTC 180
QY 181 ATCTCTGGCTCTCTGAGCGGCGCTTGTAGTCCGCCACCTGCTGCTCTGGCCACCC 240
DB 181 ATCTCTGGCTCTCTGAGCGGCGCTTGTAGTCCGCCACCTGCTGCTCTGGCCACCC 240
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DB 241 TGGGTGTGGAGTGTGCGCGGCTGCTTCTGCTTCCGCGCTGCGCGGATTCCTCCAG 300
QY 301 CGCTGTGGAGCTGTGTGGGGATGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 CGCTGTGGAGCTGTGTGGGGATGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 GGGACTGCTGAAGCAACTGGGCAAGGAGCAATGGAGTGCCTCCAGCCCTGATCGT 420
DB 361 GGGACTGCTGAAGCAACTGGGCAAGGAGCAATGGAGTGCCTCCAGCCCTGATCGT 420
QY 421 GCACCCCGCAGCGCGGATGCCAGCGGCTCAAGTCAACCATGGGAGCAGCTTCAGC 480
DB 421 GCACCCCGCAGCGCGGATGCCAGCGGCTCAAGTCAACCATGGGAGCAGCTTCAGC 480
QY 481 TACCCCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTTACCCGAGGCGCCACCTCCCA 540
DB 481 TACCCCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTTACCCGAGGCGCCACCTCCCA 540
QY 541 GCCCTGTATGCGGACTCTGCTCAAGGAGCCACTGGCCGATCCGCCACCCCATGGCAGAC 600
DB 541 GCCCTGTATGCGGACTCTGCTCAAGGAGCCACTGGCCGATCCGCCACCCCATGGCAGAC 600
QY 601 AGCTTCCCGCAGCACCTTTGCCAGTAGTCTGTGGTCCGAGGAGTACTATTCTTTCCAT 660
DB 601 AGCTTCCCGCAGCACCTTTGCCAGTAGTCTGTGGTCCGAGGAGTACTATTCTTTCCAT 660
QY 661 GAGTCGAGCTGACCTGCGGAGATGGGAGTGGCTTCCATGCTGAGCCGAGAAATTGAT 720
DB 661 GAGTCGAGCTGACCTGCGGAGATGGGAGTGGCTTCCATGCTGAGCCGAGAAATTGAT 720
QY 721 GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTGAGCGGTACACCATGATCGATGAGCTGGCC 780

Db 721 GTGCTCATCTTCAAGAAGCTGACAGAGCTGTTGAGCGGTACACCATGATCGATGAGCTGGCC 780
QY 781 AAGTGACATCAGACACTGTGTTCCTGGAGAGACCAAGATCTCGGACCTTATCAGC 840
Db 781 AAGTGACATCAGACACTGTGTTCCTGGAGAGACCAAGATCTCGGACCTTATCAGC 840
QY 841 AGCATCACCAGGACTTACCACCTGGATGAGCAGGATGCTGAGGGCGCCTGTGTCACGGC 900
Db 841 AGCATCACCAGGACTTACCACCTGGATGAGCAGGATGCTGAGGGCGCCTGTGTCACGGC 900
QY 901 ATCATTTCGCAATTAGTACCCGAAAGAGCCGTGCTCGCCACAGACCTCGGAGGGTCTTCA 960
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QY 1081 ATGCCCCGGAAGCTGAGGCGCTTATGAGGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 1140
Db 1081 ATGCCCCGGAAGCTGAGGCGCTTATGAGGCTCCAGGGTACCCAGCAAGCCATGACTCATCC 1140
QY 1141 TTCCAGGGCACCGACACAGACTGCTCGGGGGCACCTTGTCCAGGTGACTGCTAA 1197
Db 1141 TTCCAGGGCACCGACACAGACTGCTCGGGGGCACCTTGTCCAGGTGACTGCTAA 1197

RESULT 3
BM460277
LOCUS
DEFINITION BM460277 975 bp mRNA linear EST 05-FEB-2002
5', mRNA sequence.
AGENCOURT 6420313 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502726
BM460277
VERSION BM460277.1 GI:18509317
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 975)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM12141 row: f column: 07
High quality sequence stop: 659.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5502726"
/issue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 43.9%; Score 752; DB 3; Length 975;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 CCACGACCTTCCAGTACTCTCGTGGCTCCGAGGAGTACTATCTTTCCATGAGTCG 666
DB 1 CCACGACCTTCCAGTACTCTCGTGGCTCCGAGGAGTACTATCTTTCCATGAGTCG 60
QY 667 GACCTGACCTGCGGAGATGGGAGTGGCTTCCATGTCGAGCGAGAAATGATGTGCTC 726
DB 61 GACCTGACCTGCGGAGATGGGAGTGGCTTCCATGTCGAGCGAGAAATGATGTGCTC 120
QY 727 ATCTTCAAGAGCTGACAGAGCTGTTTCAGCGTACACAGATCATGAGCTGGCCAAATGC 786
DB 121 ATCTTCAAGAGCTGACAGAGCTGTTTCAGCGTACACAGATCATGAGCTGGCCAAATGC 180
QY 787 ACATCAGACCTGTTTCCCTGGAGAGACCAAGTAAAGTCTCGACCTTATCAGCAGATC 846
DB 181 ACATCAGACCTGTTTCCCTGGAGAGACCAAGTAAAGTCTCGACCTTATCAGCAGATC 240
QY 847 ACCGAGACTACCACTGGATGAGCAGGATGCTGAGGGCGCTTGGTACCGGCATCAT 906
DB 241 ACCGAGACTACCACTGGATGAGCAGGATGCTGAGGGCGCTTGGTACCGGCATCAT 300
QY 907 CGATTAGTACCCGAAAGACCGTGTGCTGCCACAGACCTCGAGGGTCTTCAACTCGG 966
DB 301 CGATTAGTACCCGAAAGACCGTGTGCTGCCACAGACCTCGAGGGTCTTCAACTCGG 360
QY 967 GCTGCTCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGT 1026
DB 361 GCTGCTCCCCAACCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGT 420
QY 1027 CTCAGCCAGATGAGCTGACAGTGCAGATCTCCAGGAGACGATGAGATGCATCGCC 1086
DB 421 CTCAGCCAGATGAGCTGACAGTGCAGATCTCCAGGAGACGATGAGATGCATCGCC 480
QY 1087 CGAAGCTGAGGCTTATGAGCTTCCAGGGTACCCAGAGCCATGATCATCTTTCCAG 1146
DB 481 CGAAGCTGAGGCTTATGAGCTTCCAGGGTACCCAGAGCCATGATCATCTTTCCAG 540
QY 1147 GGACCCGACAGACTGCTGGGGGACCCCTTGTCTCAGGTGACTGCTTACCCCTGCCA 1206
DB 541 GGACCCGACAGACTGCTGGGGGACCCCTTGTCTCAGGTGACTGCTTACCCCTGCCA 600
QY 1207 GGCCAGCTGCCACACCTTCTGGGAGAGCATGGCTTACAGATGAAGAGGGGACCA 1266
DB 601 GGCCAGCTGCCACACCTTCTGGGAGAGCATGGCTTACAGATGAAGAGGGGACCA 660
QY 1267 GGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCACATCTGGCTCTCTCTGCTT 1326
DB 661 GGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCACATCTGGCTCTCTCTGCTT 720
QY 1327 GGCTGACTGGGTCTCGGACCATGTGCATTTC 1358
DB 721 GGCTGACTGGGTCTCGGACCATGTGCATTTC 752

RESULT 4

BQ691555
LOCUS BQ691555.1
DEFINITION BQ691555.1 GI:21816871
VERSION BQ691555.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 917)

AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>;
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LCM2390 row: 0 column: 22
High quality sequence stop: 535.

FEATURES

source

1..917
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6249453"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 110"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 37.1%; Score 635; DB 5; Length 917;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCGGCTTGGAACCCCGCCCGAGCATCTGGGCTTCCAGCTTGGGACCGTGGGAG 60
DB 44 ATGCCCGGCTTGGAACCCCGCCCGAGCATCTGGGCTTCCAGCTTGGGACCGTGGGAG 103
QY 61 CGGCCAACAGAGCTATGCTGGAGACATATGATAAACCACTCAGCCCCCACCAGCCGC 120
DB 104 CGGCCAACAGAGCTATGCTGGAGACATATGATAAACCACTCAGCCCCCACCAGCCGC 163
QY 121 CGCACCCGTAGACACAGACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCATTTACCTTC 180
DB 164 CGCACCCGTAGACACAGACCCCAAGGACCTTGGCCACCATGGGCCAGAGAGCATTTACCTTC 223
QY 181 ATCTTGGCTCTGCTGAGCGGGCCCTTGAGTGTCCCCCACTGCTGCTGCTGCGGACCC 240
DB 224 ATCTTGGCTCTGCTGAGCGGGCCCTTGAGTGTCCCCCACTGCTGCTGCTGCGGACCC 283
QY 241 TGGGTGTGGAGTGTGTCGGGGCTGCTTCTGCTTCCGGCTGCGCGGATTCCTCCAG 300
DB 284 TGGGTGTGGAGTGTGTCGGGGCTGCTTCTGCTTCCGGCTGCGCGGATTCCTCCAG 343
QY 301 CGCTGTGAGCCCTGTGTGGGGGATGCAGCCCCCTGCTGTCTACTGAGGACTCCACTGAG 360
DB 344 CGCTGTGAGCCCTGTGTGGGGGATGCAGCCCCCTGCTGTCTACTGAGGACTCCACTGAG 403
QY 361 GGGACTGTGAAGCCAACTGGGCGCAAGGAGCAAAATGGAGTGTCCCGGACCGCTGTATCGT 420
DB 404 GGGACTGTGAAGCCAACTGGGCGCAAGGAGCAAAATGGAGTGTCCCGGACCGCTGTATCGT 463
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DB 464 GCACCCCGGAGCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGACGAGCTTCAGC 523
QY 481 TACCCCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTTACCGGAGGGCACCTCCCCA 540
DB 524 TACCCCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTTACCGGAGGGCACCTCCCCA 593

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QY 541 GCCCTGATCGGACCTCTGCTCAAGGAGCCACTGGCGATCCGCCAACCCATGCGACAC 600
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RESULT 5
BM823479 622 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0094733 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-102-H01
DEFINITION 5', mRNA sequence.
ACCESSION BM823479 GI:19179892
VERSION BM823479
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 622)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 102 row: H column: 01
High quality sequence stop: 622.

FEATURES
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/lab_host="DH10B"
/clone_lib="S22SNU16n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EGOR1;
Site 2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Ronald, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

ORIGIN
Query Match 36.3%; Score 622; DB 3; Length 622;
Best Local Similarity 100.0%; Pred. No. 3e-308;
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 874 GATGCTGAGGCGCGCTGTGACCGGCATCTTCGATTTAGTACCGAAGAGCCGTGCT 933
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QY 934 CGCCCCACAGACCTCGGAGGGTCTTCAACTCGGGCTGCTGCCCAACCGTGTGCCCCCT 993
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Db 121 CGCCACAGACCTCGAGGGTCTTTCAACTCGGGCTGCTGCCCAACCGCTGCTGCCCT 180
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QY 1414 GGCGCCCTTCTCTCTGCTCAT 1435
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RESULT 6
LOCUS CN289134 753 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700599935935 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN289134
VERSION CN289134.1 GI:47305548
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 753)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Pang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 753 Std Error: 0.00.
FEATURES
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1..753
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/db_xref="taxon:9606"
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line"
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/note="oligo dT primed, full-length enriched cDNA library
```


Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.D., Geoghegan, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Bednari, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrite, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
7566098

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M3 Reverse.

FEATURES
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1..510
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/tissue_type="colon"
/cell_type="KM12SM"
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II"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.4e-250;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 CTCACGCGTGTGGAGCCTGTGTGGGGGATGCGCCCTGCTGTACTGAGGACTCC 354
Db 1 CTCACGCGTGTGGAGCCTGTGTGGGGGATGCGCCCTGCTGTACTGAGGACTCC 60

QY 355 ACTGAGGGAGCTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCTCCAGCCCT 414
Db 61 ACTGAGGGAGCTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCTCCAGCCCT 120

QY 415 GATCGTGCACCCCCACCGCGGGGATGCGCAGCGGCTCAAGTCAACCATGGGAGCAGC 474
Db 121 GATCGTGCACCCCCACCGCGGGGATGCGCAGCGGCTCAAGTCAACCATGGGAGCAGC 180

QY 475 TTCAGTACCCGATGTTAAGCTCAAGGCATCCCTGTATCCCTACCGAGGGCCACC 534
Db 181 TTCAGTACCCGATGTTAAGCTCAAGGCATCCCTGTATCCCTACCGAGGGCCACC 240

QY 535 TCCACAGCCCTGATCGGACTCCTCTGCAAGGAGCCACTGGCCGATCCCCACCCCATG 594
Db 241 TCCACAGCCCTGATCGGACTCCTCTGCAAGGAGCCACTGGCCGATCCCCACCCCATG 300

QY 595 CGACACAGCCTGCCACAGCCTTTTGGCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCT 654
Db 301 CGACACAGCCTGCCACAGCCTTTTGGCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCT 670

QY 655 TTCCATGAGTCGACCTGGACCTGCGGAGATGGCAGTGGCTCCATGTGCGAGCCGAGAA 714
Db 361 TTCCATGAGTCGACCTGGACCTGCGGAGATGGCAGTGGCTCCATGTGCGAGCCGAGAA 420

QY 715 ATTGATGTGCTCATCTTCAAGAAGCTGACAGAGCTGTTTTCAGCGTACACAGATCGATGAG 774
Db 421 ATTGATGTGCTCATCTTCAAGAAGCTGACAGAGCTGTTTTCAGCGTACACAGATCGATGAG 480

QY 775 CTGGCCAAAGTCACATCATCAGACACTGTGTTTC 804
Db 481 CTGGCCAAAGTCACATCATCAGACACTGTGTTTC 510

RESULT 9
DQ045549 1181 bp DNA linear GSS 02-JUN-2005
LOCUS Pan troglodytes FLJ34633 gene, VIRTUAL TRANSCRIPT, partial
DEFINITION sequence, genomic survey sequence.
ACCESSION DQ045549
VERSION DQ045549.1 GI:66896764
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pan.
REFERENCE 1 (bases 1 to 1181)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1181)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

FEATURES
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/mol_type="genomic DNA"
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Query Match 28.7%; Score 491; DB 11; Length 1181;
Best Local Similarity 99.8%; Pred. No. 9.6e-241;
Matches 541; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 640 GAGGAGTACTATTCTTTTCATGATCGGACCTGCGGAGATGGGAGTGGCTCC 699
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QY 700 ATGTGCGCGGAGAAATTGATGTGCTCATCTTCAAGAAGCTGACAGAGCTGTTACCGGTA 759
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QY 760 CACCATGATCGATGAGCTGGCCAAAGTGCAATCAGACACTGTGTCTCTGGAGAGACAGT 819
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QY 820 AAGATCTCGGACCTTATCATGACAGCATCAGCAGGACTACACCTGGATGAGCAGGATGCT 879
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Db 820 AAGATCTCGGACCTTATCAGCAGCATCAGCAGGACTACCACTGGATGAGCAGGATGCT 879
Qy 880 GAGGCGCGCTGTGATCCGGGATCATCTGCGATTAGTACCCGAAAGACCGGTGTCGCCCA 939
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Qy 940 CAGACCTCGGAGGGTCTTCAACTCGGGCTGCTGCCCAACCCGCTGTGCGCCCTGACAGT 999
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Qy 1000 GGCCATGAGACCATGTGTGGGCTCAGGTCTCAGCCAGGATGAGTGCAGATGTCCTCC 1059
Db 1000 GGCCATGAGACCATGTGTGGGCTCAGGTCTCAGCCAGGATGAGTGCAGATGTCCTCC 1059
Qy 1060 CAGGAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1119
Db 1060 CAGGAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1119
Qy 1120 CCAGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1179
Db 1120 CCAGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1179
Qy 1180 CT 1181
Db 1180 CT 1181

RESULT 10
AI925416/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN

AI925416 489 bp mRNA linear EST 08-MAR-2000
w030a02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2456810 3',
mRNA sequence.
AI925416
AI925416.1 GI:5661380
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 489)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-x@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 831 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 432.
Location/Qualifiers
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/clone_lib="NCI_CGAP Gas4"
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

Query Match 28.0%; Score 480; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.1e-235;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1217 CCACACCCCTTCTGGGAGGAGCATGCGCTACAGAAATGAAGAGGGGACCAAGACCCCTG 1276
Db 489 CCACACCCCTTCTGGGAGGAGCATGCGCTACAGAAATGAAGAGGGGACCAAGACCCCTG 430
Qy 1277 TGGGAGAGGCTTAGAGCTGAAGCAGTGCCTCCTCTGCTCTCTCTCTCTCTCTCTCTCT 1336
Db 429 TGGGAGAGGCTTAGAGCTGAAGCAGTGCCTCCTCTCTCTCTCTCTCTCTCTCTCTCT 370
Qy 1337 GTTCTTGGACCATGTGCATTTTCACTGGGCCATGGATCTACATCTCTCTGATCCCCAGC 1396
Db 369 GTTCTTGGACCATGTGCATTTTCACTGGGCCATGGATCTACATCTCTCTGATCCCCAGC 310
Qy 1397 TGGTCTGATCCCTGCCAGGCGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1456
Db 309 TGGTCTGATCCCTGCCAGGCGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 250
Qy 1457 TGGAAAGTAAAGGATTAAGCATTTACCTTCTGGGAGTGAACCTGACTCCATCCCCCTATT 1516
Db 249 TGGAAAGTAAAGGATTAAGCATTTACCTTCTGGGAGTGAACCTGACTCCATCCCCCTATT 190
Qy 1517 GCCACCTTAACCAATCATGCAAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1576
Db 189 GCCACCTTAACCAATCATGCAAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 130
Qy 1577 GCTTATCTTAAATGATTTATTTGGGGGTGGGAGGCCCACTCTATGTTAGTTAAGG 1636
Db 129 GCTTATCTTAAATGATTTATTTGGGGGTGGGAGGCCCACTCTATGTTAGTTAAGG 70
Qy 1637 AGTTGGTCTTGGTCTTGGCTGATGTTCTGATCTTAAACATGACCACAGTTTGTAGTAC 1696
Db 69 AGTTGGTCTTGGTCTTGGCTGATGTTCTGATCTTAAACATGACCACAGTTTGTAGTAC 10

RESULT 11
BX110746/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN

BX110746 470 bp mRNA linear EST 07-FEB-2003
BX110746 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:998E036110 ;
IMAGE:2456810, mRNA sequence.
BX110746
BX110746.1 GI:27836587
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 470)
Radelof, J., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, J., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Contact: Ina Rolfs
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE:998E036110.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972)
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: GTTGTAAACACGCGCCAGT.
Location/Qualifiers

FEATURES


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/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

ORIGIN
Query Match 26.3%; Score 450; DB 5; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.1e-219;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1247 CAGAAATGAGAGGGGACCAAGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCC 1306
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QY 470 CAGAAATGAGAGGGGACCAAGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTGCC 411
Db |||||||

QY 1307 ACTCTGGCTCCTCCTGCTGACTGGGTTCCTGGACCATGTGCACTTTCACCTGGGCC 1366
Db |||||||
QY 410 ACTCTGGCTCCTCCTGCTGCTGACTGGGTTCCTGGACCATGTGCACTTTCACCTGGGCC 351
Db |||||||

QY 1367 ATGGGATACATCTCTCTGCAATCCCAAGCTGGTCTGATCCCTGCCAGGGCCCTTCCTT 1426
Db |||||||
QY 350 ATGGGATACATCTCTCTGCAATCCCAAGCTGGTCTGATCCCTGCCAGGGCCCTTCCTT 291
Db |||||||

QY 1427 CTGTCTCATGCTTTCAGTGGCTCATCATGGAAGTAGGAGTTAGGCATTTACCTTCT 1486
Db |||||||
QY 290 CTGTCTCATGCTTTCAGTGGCTCATCATGGAAGTAGGAGTTAGGCATTTACCTTCT 231
Db |||||||

QY 1487 GGGAGTGAACCTGACTCCATCCCTTATTTGCCACCTTAACCAATCATGCAAACTTCTCC 1546
Db |||||||
QY 230 GGGAGTGAACCTGACTCCATCCCTTATTTGCCACCTTAACCAATCATGCAAACTTCTCC 171
Db |||||||

QY 1547 CTCCTGGGGTAAATCAACAGTTAAAGAGCTTATCTTAATGTTATGTTGGGGGT 1606
Db |||||||
QY 170 CTCCTGGGGTAAATCAACAGTTAAAGAGCTTATCTTAATGTTATGTTGGGGGT 111
Db |||||||

QY 1607 GGGAGGGCCCACTCTATGTTATGTTAAAGAGTTGGTCTCTGTTCTGATGTTCTG 1666
Db |||||||
QY 110 GGGAGGGCCCACTCTATGTTATGTTAAAGAGTTGGTCTCTGTTCTGTTCTGTTCTG 51
Db |||||||

QY 1667 TATCTTAAACATGACCAAGTTTGTAAAGTAC 1696
Db |||||||
QY 50 TATCTTAAACATGACCAAGTTTGTAAAGTAC 21
Db |||||||

RESULT 12
BE901537
LOCUS BE901537
DEFINITION 601677420F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960220 5',
mrna sequence.
ACCESSION BE901537
VERSION BE901537.1 GI:10390818
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 966)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM842 row: 9 column: 05
High quality sequence stop: 668.

FEATURES
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/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; CDNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

Query Match 26.3%; Score 450; DB 2; Length 966;
Best Local Similarity 100.0%; Pred. No. 1.2e-219;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 CACCATGGGCCAGAGAGCATTAACCTTCATCTGTGGCTCTGTGAGCGCGCCCTTGAGTCC 213
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QY 59 CACCATGGGCCAGAGAGCATTAACCTTCATCTGTGGCTCTGTGAGCGCGCCCTTGAGTCC 118
Db |||||||

QY 214 CCCACCTGTCTGCTCTGTGGGACCCCTGGGTGTGGAGTGTGCGGGCTGCTTCTGC 273
Db |||||||

QY 119 CCCACCTGTCTGCTCTGTGGGACCCCTGGGTGTGGAGTGTGCGGGCTGCTTCTGC 178
Db |||||||

QY 274 TTCCGGCGCTGCGGGATTTCCCTCCAGCGCTGTGAGCGCTGTGTGCGGGATGACGCCCC 333
Db |||||||

QY 179 TTCCGGCGCTGCGGGATTTCCCTCCAGCGCTGTGTGAGCGCTGTGTGCGGGATGACGCCCC 238
Db |||||||

QY 334 TGCCTGTCTACTGAGGACTCCACTGAGGGGACTGTCTGAAGCCAACTGGGCGCAAGAGGAC 393
Db |||||||

QY 239 TGCCTGTCTACTGAGGACTCCACTGAGGGGACTGTCTGAAGCCAACTGGGCGCAAGAGGAC 298
Db |||||||

QY 394 AATGAGTGTCCCGCCAGCCCTGATCGTGACCCCGCGGGGATGCGCAGCGGCTC 453
Db |||||||

QY 299 AATGAGTGTCCCGCCAGCCCTGATCGTGACCCCGCGGGGATGCGCAGCGGCTC 358
Db |||||||

QY 454 AAGTCAACCATGGGACGAGCTTTCAGCTACCCCGATGTTAAGCTCAAGGCACTCCCTGTG 513
Db |||||||

QY 359 AAGTCAACCATGGGACGAGCTTTCAGCTACCCCGATGTTAAGCTCAAGGCACTCCCTGTG 418
Db |||||||

QY 514 TATCCCTACCCGAGGGCCACCTCCCGAGCCCTGATGCGGACTCTCTGTGCAAGAGGCCA 573
Db |||||||

QY 419 TATCCCTACCCGAGGGCCACCTCCCGAGCCCTGATGCGGACTCTCTGTGCAAGAGGCCA 478
Db |||||||

QY 574 CTGGCCGATCCCGCCACCCATGGGACACAGC 603
Db |||||||

QY 479 CTGGCCGATCCCGCCACCCATGGGACACAGC 508
Db |||||||

RESULT 13
BP331524
LOCUS BP331524
DEFINITION BP331524 Sugano cDNA library, rectum Homo sapiens cDNA clone
R209504, mRNA sequence.
ACCESSION BP331524
VERSION BP331524.1 GI:52260875
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
JOURNAL
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
FEATURES
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1. 583
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/db_xref="taxon:9606"
/clone="R0109504"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.9e-206;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 TGTCTGAGACATATGATAAACCACCTCAGCCGCCCAAGCGCGCCGCTAGACCA 135
DB 59 TGTCTGAGACATATGATAAACCACCTCAGCCGCCCAAGCGCGCCGCTAGACCA 118
QY 136 GACCCCAAGGACCTTGGCCCAACCATGGCCCGAGAGCATTTACCTTCTGCTCTGCT 195
DB 119 GACCCCAAGGACCTTGGCCCAACCATGGCCCGAGAGCATTTACCTTCTGCTCTGCT 178
QY 196 GAGCGCGCCCTTGAAGTCCCGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
DB 179 GAGCGCGCCCTTGAAGTCCCGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 238
QY 256 TGCCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
DB 239 TGCCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 298
QY 316 GTGCGGGGATGAGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 375
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QY 376 AACTGGGCCAAGGAGCAATGAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435
DB 359 AACTGGGCCAAGGAGCAATGAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
QY 436 CGGGATGGCCAGCGGCTCAAGTCAACCATGGGAGGAGCTTCAAGTCAACCATGGGAGGAGCTT 495
DB 419 CGGGATGGCCAGCGGCTCAAGTCAACCATGGGAGGAGCTTCAAGTCAACCATGGGAGGAGCTT 478
QY 496 CTCA 499
DB 479 CTCA 482
RESULT 14
AW589267/c
LOCUS
DEFINITION
x27g07.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2770908 3',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.
1 (bases 1 to 370)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 361.
Location/Qualifiers
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1. 370
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/db_xref="taxon:9606"
/clone="IMAGE:2770908"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ut2"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI. Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"
ORIGIN
Query Match 21.6%; Score 370; DB 1; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.8e-178;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1327 GGCTGACTGGGTTCTCGACCATGTGCATTTCACTGGGCCATGGGATCTACATCTCCTTG 1386
DB 370 GGCTGACTGGGTTCTCGACCATGTGCATTTCACTGGGCCATGGGATCTACATCTCCTTG 311
QY 1387 CATCCCGAGCTGTGTGATCCCTGCCAGGCGCCCTTCTCTCTGCTCATGGTCTTCAAGT 1446
DB 310 CATCCCGAGCTGTGTGATCCCTGCCAGGCGCCCTTCTCTCTGCTCATGGTCTTCAAGT 251
QY 1447 GGCTGATCATGAAAGTAGGAGTTAGGCATTTACCTTCTGGGAGTGAAACCTGACTCCA 1506
DB 250 GGCTGATCATGAAAGTAGGAGTTAGGCATTTACCTTCTGGGAGTGAAACCTGACTCCA 191
QY 1507 TCCCTCTATTGCCACCTTAACCAATCATGCAAACTTCTCTCTCTCTGGGGTAAATTCACA 1566
DB 190 TCCCTCTATTGCCACCTTAACCAATCATGCAAACTTCTCTCTCTGGGGTAAATTCACA 131
QY 1567 GTTAAAGAGCTTATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1626
DB 130 GTTAAAGAGCTTATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 71
QY 1627 TATGTTAAGGAGTGTGTTCTTGGTCTGATGTTCTGATCTTAAATGATGATGATGATGATGAT 1686
DB 70 TATGTTAAGGAGTGTGTTCTTGGTCTGATGTTCTGATCTTAAATGATGATGATGATGATGAT 11
QY 1687 TTGTAAGTAC 1696
DB 10 TTGTAAGTAC 1
RESULT 15
CD702656
LOCUS
DEFINITION
ACCESSION
VERSION
CD702656.1 GI:32233286
CD702656 513 bp mRNA linear EST 25-JUN-2003
EST19181 human nasopharynx Homo sapiens cDNA, mRNA sequence.

KEYWORDS	EST.	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
SOURCE	Homo sapiens (human)	Tumor Gene Index
ORGANISM	Homo sapiens	Unpublished (1997)
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Contact: Robert Strausberg, Ph.D.
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	Email: cgapsb@mail.nih.gov
	Hominidae; Homo.	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
REFERENCE	1 (bases 1 to 513)	Emmert-Buck, M.D., Ph.D.
AUTHORS	Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.	CDNA Library Preparation: M. Bento Soares, Ph.D.
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx	CDNA Library Arrayed by: Greg Lennon, Ph.D.
JOURNAL	Unpublished (2003)	DNA Sequencing by: Washington University Genome Sequencing Center
COMMENT	Contact: Yixin Zeng	Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
	Cancer Center	Insert Length: 236 Std Error: 0.00
	Sun Yat-sen University	Seq primer: -40UP from Gibco.
	651 Dongfeng Road East, Guangzhou 510060, China	Location/Qualifiers
	Tel: 86-1380-9770-743	1. .513
	Fax: 86-20-8775-4506	/organism="Homo sapiens"
FEATURES	Email: yxzeng@zsums.edu.cn.	/mol_type="mRNA"
source	Location/Qualifiers	/db_xref="taxon:9606"
	1. .513	/clone="IMAGE:2296223"
	/organism="Homo sapiens"	/lab_host="DH10B"
	/mol_type="mRNA"	/lab_lib="NCI CGAP Kid11"
	/db_xref="taxon:9606"	/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."
ORIGIN	library from southern Chinese	
	Query Match 18.9%; Score 323; DB 6; Length 513;	
	Best Local Similarity 100.0%; Pred. No. 3e-154;	
	Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1115 GGTACCCAGAACCATGACTATCTTCCAGGGCACCCACACAGACTCGTCGGGGGCAC 1174	
Db	74 GGTACCCAGAACCATGACTATCTTCCAGGGCACCCACACAGACTCGTCGGGGGCAC 133	
QY	1175 CTTGTCTCAGGTGTACTGTAACCCCTGCAGGCCAGCTGCCACACCCCTTCTGGGAG 1234	
Db	134 CTTGTCTCAGGTGTACTGTAACCCCTGCAGGCCAGCTGCCACACCCCTTCTGGGAG 193	
QY	1235 AAGCATGGCTACAGAAATGAAGAGGGGACACAGAAACCCCTGTGGGAGAGGCTTAGACCT 1294	
Db	194 AAGCATGGCTACAGAAATGAAGAGGGGACACAGAAACCCCTGTGGGAGAGGCTTAGACCT 253	
QY	1295 GAAGCATGCCCCACTCTGGCTCTCTCTGCTTGGCTGACTGGGTTCTGGACCATGTGCA 1354	
Db	254 GAAGCATGCCCCACTCTGGCTCTCTCTGCTTGGCTGACTGGGTTCTGGACCATGTGCA 313	
QY	1355 TTTCACCTGGCCATGGATCTACATCTCTTGCATCCCGAGCTGGTCTGATCCCTGCCAG 1414	
Db	314 TTTCACCTGGCCATGGATCTACATCTCTTGCATCCCGAGCTGGTCTGATCCCTGCCAG 373	
QY	1415 GGCCCTCTCTCTCTCTCTCATGG 1437	
Db	374 GGCCCTCTCTCTCTCTCATGG 396	
RESULT 16		
AI702452/c	330 bp mRNA linear EST 16-DEC-1999	
LOCUS	tz94b12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296223 3',	
DEFINITION	mRNA sequence.	
ACCESSION	AI702452	
VERSION	AI702452.1 GI:4990352	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
REFERENCE	1 (bases 1 to 330)	
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
JOURNAL	Tumor Gene Index	
COMMENT	Unpublished (1997)	
	Contact: Robert Strausberg, Ph.D.	
	Email: cgapsb@mail.nih.gov	
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.	
	Emmert-Buck, M.D., Ph.D.	
	CDNA Library Preparation: M. Bento Soares, Ph.D.	
	CDNA Library Arrayed by: Greg Lennon, Ph.D.	
	DNA Sequencing by: Washington University Genome Sequencing Center	
	Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html	
	Insert Length: 236 Std Error: 0.00	
	Seq primer: -40UP from Gibco.	
FEATURES	Location/Qualifiers	
source	1. .330	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:2296223"	
	/lab_host="DH10B"	
	/lab_lib="NCI CGAP Kid11"	
	/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."	
ORIGIN		
	Query Match 18.7%; Score 321; DB 1; Length 330;	
	Best Local Similarity 100.0%; Pred. No. 3.1e-153;	
	Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1376 ACATCTCTTGCATCCCGAGCTGTGATCCTCGCAGGGCCCTTCTCTCTGCTCAT 1435	
Db	330 ACATCTCTTGCATCCCGAGCTGTGATCCTCGCAGGGCCCTTCTCTCTGCTCAT 271	
QY	1436 GGTCTTCAGTGGCTGATCATGGAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAA 1495	
Db	270 GGTCTTCAGTGGCTGATCATGGAAGTAAGAGTTAGGCATTACCTTCTGGAGTGAA 211	
QY	1496 CCTGACTCATCCCTTATTCACCCCTTAACCAATCATGCAAACTTCTCCCTCCCTGG 1555	
Db	210 CCTGACTCATCCCTTATTCACCCCTTAACCAATCATGCAAACTTCTCCCTCCCTGG 151	
QY	1556 GTAATTCAACAGTAAAGAAGCTTATCTTAATGTATTGTTGGGGGTGGCGAGGC 1615	
Db	150 GTAATTCAACAGTAAAGAAGCTTATCTTAATGTATTGTTGGGGGTGGCGAGGC 91	
QY	1616 CCACCTATGTATTGTTAAAGGAGTTGGTCTCGTCTTCTGGCTGATGTTCTGTATCTTAAC 1675	
Db	90 CCACCTATGTATTGTTAAAGGAGTTGGTCTCGTCTTCTGGCTGATGTTCTGTATCTTAAC 31	
QY	1676 ATGACCACAGTTTGTAAAGTAC 1696	
Db	30 ATGACCACAGTTTGTAAAGTAC 10	
RESULT 17		
BE741035	1015 bp mRNA linear EST 15-SEP-2000	
LOCUS	601594018F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947861 5',	
DEFINITION	mRNA sequence.	
ACCESSION	BE741035	
VERSION	BE741035.1 GI:1015027	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1015)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLC810 row: d column: 06
High quality sequence stop: 752.

FEATURES
source Location/Qualifiers
1..1015
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3947861"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/notes="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 17.7%; Score 303; DB 2; Length 1015;
Best Local Similarity 99.5%; Pred. No. 6.4e-144;
Matches 403; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 204 CCTTGAGTCCCCACCTGCTGCTCTGGCGACCTGGGTGGAGTGGTGGCGGC 263
DB 147 CCTTGAGTCCCCACCTGCTGCTCTGGCGACCTGGGTGGAGTGGTGGCGGC 206
QY 264 TGCCTTCTGCTTCCGCGCTGCGCGGATTGCTCCAGCGCTGTGGAGCTGTGTGGGG 323
DB 207 TGCCTTCTGCTTCCGCGCTGCGCGGATTGCTCCAGCGCTGTGGAGCTGTGTGGGG 266
QY 324 ATGACGCCCCCTGCTGTCTACTAGGACTCCATGAGGGGACTGCTGGAAGCCAACTGGGC 383
DB 267 ATGACGCCCCCTGCTGTCTACTAGGATTCCATGAGGGGACTGCTGGAAGCCAACTGGGC 326
QY 384 CAAAGGACCAATGGAGTGGCCCGACCTGATCGTGCACCCCGCCAGCGCGGGATGG 443
DB 327 CAAAGGACCAATGGAGTGGCCCGACCTGATCGTGCACCCCGCCAGCGCGGGATGG 386
QY 444 CCAGCGGCTCAAGTCAACATGGGACAGCAGCTTCAGTACCCCGCTGTTAAGCTCAAAGG 503
DB 387 CCAGCGGCTCAAGTCAACATGGGACAGCAGCTTCAGTACCCCGCTGTTAAGCTCAAAGG 446
QY 504 CATCCCTGTGTATCCCTTACCCAGGGGCCACCTCCCGAGCCCTGTATGCGGACTCTCTGCTG 563
DB 447 CATCCCTGTGTATCCCTTACCCAGGGGCCACCTCCCGAGCCCTGTATGCGGACTCTCTGCTG 506
QY 564 CAAAGGACCAATGGAGTGGCCCGACCTGATCGGACAGCAGCTGCC 608
DB 507 CAAAGGACCAATGGAGTGGCCCGACCTGATCGGACAGCAGCTGCC 551

RESULT 18
AA573775/c LOCUS

DEFINITION nk07d10.s1 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1012819 3',
mRNA sequence.
AA573775
VERSION AA573775.1 GI:2348290
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 556)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
Ph.D.
CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 635 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 465.

FEATURES
source Location/Qualifiers
1..556
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1012819"
/tissue_type="tumor"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="NCI_CGAP_Co2"
/notes="Organ: colon; Vector: Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Bulk colon villous adenoma. 5' adaptor sequence:
5' GAATTCGGCAGCG 3' 3' adaptor sequence: 5'
CTCAGATTTTTTTTTTTTTTTT 3' Average insert size: 1.1 kb."

ORIGIN
Query Match 17.0%; Score 291; DB 1; Length 556;
Best Local Similarity 99.6%; Pred. No. 9.1e-138;
Matches 461; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1141 TTCCAGGGCACCGACACAGACTCGTCGGGGGACCCCTTGTCTCCAGGTGTACTGTACCC 1200
DB 556 TTCCAGGGCACCGACACAGACTCGTCGGGGGACCCCTTGTCTCCAGGTGTACTGTACCC 497
QY 1201 CTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCCTACAGATCAAGAGGG 1260
DB 496 CTGCCAGGCCAGCTGCCACACCCCTTCTGGGAGAGCATGGCCTACAGATCAAGAGGG 437
QY 1261 GGACACAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCTCTGCTCTCC 1320
DB 436 GGACACAGGAACCCCTGTGGGAGAGGCTTAGACCTGAAGCAGTGCCTCTGCTCTCC 377
QY 1321 TGCCTTGGCTGACTGGGTTCTTGACCATGTGCAATTTC-ACTGGGCCATGGGATCTACAT 1379
DB 376 TGCCTTGGCTGACTGGGTTCTTGACCATGTGCAATTTC-ACTGGGCCATGGGATCTACAT 317
QY 1380 CTCTTGGCATCCCGAGCTGCTGATCCCTGCCAGGGCCCTCTCTCTCTGCTCATGGTC 1439
DB 316 CTCTTGGCATCCCGAGCTGCTGATCCCTGCCAGGGCCCTCTCTCTCTGCTCATGGTC 257
QY 1440 TTCAGGTGGCTGATCATGGAAGTAAGGAGTTAGGCATTTACCTCTCTGGAGTGAACCT 1499
DB 256 TTCAGGTGGCTGATCATGGAAGTAAGGAGTTAGGCATTTACCTCTCTGGAGTGAACCT 197


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QY 1491 GTGAACCTGACTCC-ATCCCCCTATTGGCCACCTCAACCAATCATGCAAACTTCTCCCTC 1549
Db 213 GTGAACCTGACTCCAAATCCCTTATTGGCCACCTCAACCAATCATGCAAACTTCTCCCTC 154
QY 1550 CCTGGGGTAATTCAACAGTTAAAGAGAGCTTATCTTAAATGTTATTGTTATTTGGGGGGTGGG 1609
Db 153 CCTGGGGTAATTCAACAGTTAAAGAGAGCTTATCTTAAATGTTATTGTTATTTGGGGGGTGGG 94
QY 1610 CAGGGCCCACTCTATGTTATTGTTAAAGAGAGTTGGTCTGGTCTTGGTCTGATGTTCTGAT 1669
Db 93 CAGGGCCCACTCTATGTTATTGTTAAAGAGAGTTGGTCTGGTCTTGGTCTGATGTTCTGAT 34
QY 1670 CTTAACAATGACCAAGTTTGTAGTAC 1696
Db 33 CTTAACAATGACCAAGTTTGTAGTAC 7
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RESULT 21
BE162756
LOCUS BE162756 244 bp mRNA linear EST 21-JUN-2000
DEFINITION PM1-HT0454-170100-003-f07 HT0454 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE162756
VERSION BE162756.1 GI:8625477
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 244)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=PM1-HT0454-170
100-003-f07&t3=2000-01-17&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 244.
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FEATURES
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /dev_stage="Adult"
            /clone_lib="HT0454"
            /note="Organ: head neck; Vector: puc18; Site:1: SmaI;
            Site:2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
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ORIGIN

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Query Match 12.4%; Score 213; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.2e-97;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 267 CTTCTGCTTCCGCGCTGCCGGATTGCTTCAGCGCTGTGAGCCTGTGTGCGGGGATG 326
Db 29 CTTCTGCTTCCGCGCTGCCGGATTGCTTCAGCGCTGTGAGCCTGTGTGCGGGGATG 88
QY 327 CAGCCCCCTGCTGTCTACTGAGGACTCCACTGAGGGGACTGCTGAAGCCAACTGGGCCAA 386
Db 89 CAGCCCCCTGCTGTCTACTGAGGACTCCACTGAGGGGACTGCTGAAGCCAACTGGGCCAA 148
QY 387 GGAGCACAATGAGTGGTCCCCCAGCCCTGATCGTGCACCCGCCAGCGGGGGATGGCCA 446
Db 149 GGAGCACAATGAGTGGTCCCCCAGCCCTGATCGTGCACCCGCCAGCGGGGGATGGCCA 208
QY 447 GCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAG 479
Db 209 GCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAG 241
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RESULT 22
BM750392
LOCUS BM750392 246 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0025949 S7SNU719 Homo sapiens cDNA clone S7SNU719-1-G12 5',
mRNA sequence.
ACCESSION BM750392
VERSION BM750392.1 GI:19080010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 246)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: G column: 12
High quality sequence stop: 246.
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FEATURES
    source
        1..246
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="S7SNU719-1-G12"
            /sex="M"
            /tissue_type="Stomach"
            /cell_type="Epithelial"
            /cell_line="SNU-719"
            /lab_host="Top10F"
            /clone_lib="S7SNU719"
            /note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;
            Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
            bacterial alkaline phosphatase (BAP) and then decapped
            with tobacco acid pyrophosphatase (TAP). The decapped
            intact mRNA was ligated with DNA-RNA linker including EcoR
            I site by treatment of T4 RNA ligase and the first strand
            cDNA was synthesized from oligo dt-selected mRNA by
            priming with dt-tailed vector. The dt-tailed vector was
            adjusted to have about 60nt. The cDNA vector was
            circularized with E. coli DNA ligase after digestion of
            EcoRI which site is also included in vector. An RNA strand
            converted to a DNA strand by Okayama-Berg method. The
            obtained cDNA vectors were used for transfection of
            competent cells E. coli Top10F' by electroporation method.
            The cDNA libraries constructed by this method are
```

full-length enriched cDNA library."

ORIGIN

Query Match 12.1%; Score 208; DB 3; Length 246;
Best Local Similarity 100.0%; Pred. No. 4.7e-95;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1489 GAGTGAACCTGACTCCATCCCTATGCGACCTTAACCAATCATGCAAACTTCCTCT 1548
|||||
DB 28 GAGTGAACCTGACTCCATCCCTATGCGACCTTAACCAATCATGCAAACTTCCTCT 87
|||||

QY 1549 CCTCTGGGTAAATCAACAGTTAAAGAAAGCTTATCTTAAATGATTTATTTGGGGGGTGG 1608
|||||

DB 88 CCTCTGGGTAAATCAACAGTTAAAGAAAGCTTATCTTAAATGATTTATTTGGGGGGTGG 147
|||||

QY 1609 GCAGGCCCACTATGTTATGTTAAGGAGTGGTCTGGTCTGGCTGATGTTCTGTA 1668
|||||

DB 148 GCAGGCCCACTATGTTATGTTAAGGAGTGGTCTGGTCTGGCTGATGTTCTGTA 207
|||||

QY 1669 TCTTACATGACCACAGTTTGTAAAGTAC 1696
|||||

DB 208 TCTTACATGACCACAGTTTGTAAAGTAC 235
|||||

RESULT 23

BG998476

LOCUS BG998476 291 bp mRNA linear EST 13-JUN-2001

DEFINITION MR4-HT1265-170401-002-d07 HT1265 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG998476

VERSION BG998476.1 GI:14402546

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 291)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-HT1265-170401-002-d07&t3=2001-04-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 284.

FEATURES

source

1. .291
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT1265"
/note="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 10.5%; Score 180; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.3e-80;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 GCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAATCAACAGTTAAAGAA 1576
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DB 60 GCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAATCAACAGTTAAAGAA 119
|||||

QY 1577 GCTTATCTTAAATGATTTATTTGGGGGTGGGAGGCCCACTCTATGTTATGTTAAGG 1636
|||||

DB 120 GCTTATCTTAAATGATTTATTTGGGGGTGGGAGGCCCACTCTATGTTATGTTAAGG 179
|||||

QY 1637 AGTTGGTCTGGTCTTCTGGCTGATGTTCTGTATCTTAAACATGACCACAGTTGTAAGTAC 1696
|||||

DB 180 AGTTGGTCTGGTCTTCTGGCTGATGTTCTGTATCTTAAACATGACCACAGTTGTAAGTAC 239
|||||

RESULT 24

BE409561

LOCUS BE409561 1092 bp mRNA linear EST 21-JUL-2000

DEFINITION BE409561 NTH_MGC_21 Homo sapiens cDNA clone IMAGE:3629848 5', mRNA sequence.

ACCESSION BE409561

VERSION BE409561.1 GI:9346011

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1092)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM317 row: a column: 17
High quality sequence start: 19
High quality sequence stop: 482.

FEATURES

source

1. .1092
Location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3629848"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 9.1%; Score 156; DB 2; Length 1092;
Best Local Similarity 100.0%; Pred. No. 3.3e-68;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 GTGGAGCGCCACAGAGCTATGCTCTGGAGACATATATATACCACTCAGCCCCCACC 113
|||||
Db 158 GTGGAGCGCCACAGAGCTATGCTCTGGAGACATATATATACCACTCAGCCCCCACC 217
|||||
QY 114 AAGCGCGCCGACCGTAGACAGACACCCCAAGGACCCCTGGCCACCATGGCCAGAGAGCAT 173
|||||
Db 218 AAGCGCGCCGACCGTAGACAGACACCCCAAGGACCCCTGGCCACCATGGCCAGAGAGCAT 277
|||||
QY 174 TACCTTCATCTCTGGCTCTGCTAGCGCGCCCTTGA 209
|||||
Db 278 TACCTTCATCTCTGGCTCTGCTAGCGCGCCCTTGA 313
|||||

RESULT 25
BE741110 623 bp mRNA linear EST 15-SEP-2000
LOCUS 601593919F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947885 5',
DEFINITION mRNA sequence.
ACCESSION BE741110
VERSION BE741110.1 GI:10155102
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 623)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM810 row: e column: 06
High quality sequence stop: 615.
Location/Qualifiers
FEATURES
source
1..623
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3947885"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/notes="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 8.5%; Score 145; DB 2; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.4e-62;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 GACCCCAAGGACCCCTGGCCACCATGGCCAGAGAGCATTTACCTTCATCTCTGGCTCTGCT 195
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Db 85 GACCCCAAGGACCCCTGGCCACCATGGCCAGAGAGCATTTACCTTCATCTCTGGCTCTGCT 144
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QY 196 GAGCCGCGCCCTTGAGTCCCCCACCCTGCTGCTCTGGCCAGCCCTGGGTGTGGAGTGG 255
|||||
Db 145 GAGCCGCGCCCTTGAGTCCCCCACCCTGCTGCTCTGGCCAGCCCTGGGTGTGGAGTGG 204
|||||

QY 256 TGCGGGCTCCTCTGCTTCGGCC 280
|||||

Db 205 TGCGGGCTCCTCTGCTTCGGCC 229
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RESULT 26
AW732798 139 bp mRNA linear EST 21-APR-2000
LOCUS bb14f07.y1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2962885 5',
DEFINITION mRNA sequence.
ACCESSION AW732798
VERSION AW732798.1 GI:7633136
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 139)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 112.
Location/Qualifiers
FEATURES
source
1..139
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2962885"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/notes="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 8.1%; Score 139; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 378 CTGGGCCAAGGACCAATGGAGTGGCCCCCAGCCCTGATCGTGACCCCGCCGCGG 437
|||||
Db 1 CTGGGCCAAGGACCAATGGAGTGGCCCCCAGCCCTGATCGTGACCCCGCCGCGG 60
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QY 438 GGATGGCCAGCGGCTCAAGTCAACCATGGCAGCAGCTTCAGTACCCCGATGTTAAGCT 497
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Db 61 GGATGGCCAGCGGCTCAAGTCAACCATGGCAGCAGCTTCAGTACCCCGATGTTAAGCT 120
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QY 498 CAAAGGCATCCCTGTGTAT 516
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Db 121 CAAAGGCATCCCTGTGTAT 139
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RESULT 27
BF856421 450 bp mRNA linear EST 16-JAN-2001
LOCUS RC0-FN0204-221200-022-b01 FN0204 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BF856421
VERSION BF856421.1 GI:12244165

KEYWORDS	EST.	Homo sapiens (human)	Homo sapiens (human)	
SOURCE	Homo sapiens	Homo sapiens	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 450)	1 (bases 1 to 277)	1 (bases 1 to 277)	
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalbo,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jorgeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.	
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	21C Frontier Korean EST Project 2001	21C Frontier Korean EST Project 2001	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Unpublished (2002)	Unpublished (2002)	
PUBMED	10737800	Contact: Kim YS	Contact: Kim YS	
COMMENT	Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC0&t2=RC0-FN0204-221200-022-b01&t3=2000-12-22&t4=1) Seq primer: puc 18 forward High quality sequence start: 72 High quality sequence stop: 446.	Email: yongsung@mail.kribb.re.kr Plate: 20 row: C column: 05 High quality sequence stop: 277.	Email: yongsung@mail.kribb.re.kr Plate: 20 row: C column: 05 High quality sequence stop: 277.	
FEATURES	Location/Qualifiers 1..450 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="FN0204" /note="Organ: prostate normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	Location/Qualifiers 1..277 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="S9SNU601-20-C05" /sex="M" /tissue_type="Ascites" /cell_type="Epithelial" /cell_line="SNU-601" /lab_host="Top10F" /clone_lib="S9SNU601" /note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	Location/Qualifiers 1..277 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="S9SNU601-20-C05" /sex="M" /tissue_type="Ascites" /cell_type="Epithelial" /cell_line="SNU-601" /lab_host="Top10F" /clone_lib="S9SNU601" /note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."	Location/Qualifiers 1..277 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="S9SNU601-20-C05" /sex="M" /tissue_type="Ascites" /cell_type="Epithelial" /cell_line="SNU-601" /lab_host="Top10F" /clone_lib="S9SNU601" /note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
ORIGIN	Query Match 6.4%; Score 109; DB 2; Length 450; Best Local Similarity 99.4%; Pred. No. 4.9e-44; Matches 159; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Query Match 5.9%; Score 101; DB 3; Length 277; Best Local Similarity 100.0%; Pred. No. 6.1e-40; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 5.9%; Score 101; DB 3; Length 277; Best Local Similarity 100.0%; Pred. No. 6.1e-40; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 5.9%; Score 101; DB 3; Length 277; Best Local Similarity 100.0%; Pred. No. 6.1e-40; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1420 CTTCTCTCTGCTCATGGTCTTCAGGTGGCGCTGATCATGGAAGTAAAGGTTAGGCATT 1479	35 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 94	35 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 94	35 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 94
Db	196 CTTCTCTCTGCTCATGGTCTTCAGGTGGCGCTGATCATGGAAGTAAAGGTTAGGCATT 255	86 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 145	86 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 145	86 GGCCTCCACGCTTGGGACCGTGGAGCGGCCAACAGAGTATGCTCTGGAGACATATGATA 145
QY	1480 ACCTCTGGGAGTGAACCTTGATCCATCCCTTATGACCCCTAACCAATCATGCAAA 1539	95 AACCACTCAGCCCCCACCAGCCGCCGCGCCGCTAGACCA 135	95 AACCACTCAGCCCCCACCAGCCGCCGCGCCGCTAGACCA 135	95 AACCACTCAGCCCCCACCAGCCGCCGCGCCGCTAGACCA 135
Db	256 ACCTCTGGGAGTGAACCTTGATCCATCCCTTATGACCCCTAACCAATCATGCAAA 315	146 AACCACTCAGCCCCCACCAGCCGCCGCGCCGCTAGACCA 186	146 AACCACTCAGCCCCCACCAGCCGCCGCGCCGCTAGACCA 186	146 AACCACTCAGCCCCCACCAGCCGCCGCGCCGCTAGACCA 186
QY	1540 CTTCTCCCTCCCTGGGTAAATCAACAGTTTAAAGAAGCT 1579			
Db	316 CTTCTCCCTCCCTGGGTAAATCAACAGTTTAAAGAAGCT 355			
RESULT 28	CR763815	CR763815	CR763815	CR763815
LOCUS	BQ081980	BQ081980	BQ081980	BQ081980
DEFINITION	K-EST0026481 S9SNU601 Homo sapiens cDNA clone S9SNU601-20-C05 5', mRNA sequence.	276 bp mRNA linear EST 23-SEP-2004	276 bp mRNA linear EST 23-SEP-2004	276 bp mRNA linear EST 23-SEP-2004
ACCESSION	BQ081980	EST.	EST.	EST.
VERSION	BQ081980.1	GI:52602277	GI:52602277	GI:52602277
KEYWORDS	EST.	Pongo pygmaeus (orangutan)	Pongo pygmaeus (orangutan)	Pongo pygmaeus (orangutan)
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pongo.
REFERENCE
AUTHORS 1 (bases 1 to 276)
        Ansoerge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
        Mewes,H.W., Weil,B., Amid,C., Oeanger,A., Fobo,G., Han,M. and
        Wiemann,S.
TITLE    Pongo pygmaeus mRNA (Ansoerge,W., Krieger,S., Regiert,T., et al.)
JOURNAL  Unpublished (2004)
COMMENT  Contact: MIPS
        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
        This is the 5' sequence of the clone insert. Clone from S. Wiemann,
        Molecular Genome Analysis, German Cancer Research Center (DKFZ);
        Email s.wiemann@kfz-heidelberg.de; riin, Germany. Please contact
        RZPD for ordering.
        http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469G0138
        Further information about the clone and the sequencing project is
        available at http://mips.gsf.de/projects/cdna/.
FEATURES
source  Location/Qualifiers
        1..276
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        /mol_type="mRNA"
        /db_xref="taxon:9600"
        /clone="DKFZp469G0138"
        /tissue_type="kidney"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="469 (synonym: pkid1)"
        /note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN
Query Match      5.7%; Score 97; DB 7; Length 276;
Best Local Similarity 99.3%; Pred. No. 7e-38;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAGCGCCACAGAGCTATGTCGGAGACATATGATAACCACTCAGCCGCCACCAAGC 117
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Db 120 GAGCGCCACAGAGCTATGTCGGAGACATATGATAACCACTCAGCCGCCACCAAGC 179

QY 118 CGCGCAGCCGCTAGACAGACCCAGGACCCCTGGCCACCATGGGCGAGAGCATTACC 177
    |||||
Db 180 CGCGCAGCCGCTAGACAGACCCAGGACCCCTGGCCACCATGGGCGAGAGCATTACC 239

QY 178 TTCACTCTGGCTCTCTCTGAGCGGCC 205
    |||||
Db 240 TTCACTCTGGCTCTCTGAGCGGCC 267

RESULT 30
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LOCUS      928 bp mRNA linear EST 27-FEB-2001
DEFINITION 602404274F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541898 5',
mRNA sequence.
ACCESSION  BG335647
VERSION     BG335647.1 GI:13142085
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 928)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA library preparation: Ling Hong/Rubin Laboratory
            cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
Plate: LLCMI221 row: c column: 19
High quality sequence stop: 496.
FEATURES
source  Location/Qualifiers
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:4541898"
        /tissue_type="choriocarcinoma"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH MGC 21"
        /note="Organ: Placenta; Vector: pOTB7; Site_1: XhoI;
        Site_2: EcoRI; cDNA made by oligo-dt priming.
        Directionally cloned into EcoRI/XhoI sites using the
        following 5' adaptor: GGCACGAG(G). Size-selected >500bp
        for average insert size 1.8kb. Library constructed by
        Ling Hong in the laboratory of Gerald M. Rubin (University
        of California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies).".
ORIGIN
Query Match      5.7%; Score 97; DB 2; Length 928;
Best Local Similarity 100.0%; Pred. No. 7.9e-38;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCGCCCTGGACACCCCGCCCGCCAGCATCTGGGCTCCACGCTTGGACCGTGGAG 60
    |||||
Db 103 ATGCCCGCCCTGGACACCCCGCCCGCCAGCATCTGGGCTCCACGCTTGGACCGTGGAG 162

QY 61 CGGCCACAGAGCTATGTCGGAGACATATGATAAAC 97
    |||||
Db 163 CGGCCACAGAGCTATGTCGGAGACATATGATAAAC 199

RESULT 31
AG071655
LOCUS      677 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-062016.F, genomic survey sequence.
ACCESSION  AG071655
VERSION     AG071655.1 GI:16623457
KEYWORDS   GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM    Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      BAC end sequences of Library PTB
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 677)
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpsgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT    Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
            PRIMERS
            Sequencing: -21M13
            LIBRARY
            Vector : pKS145
            R.Site 1 : SacI
            R.Site 2 : SacI.
            Location/Qualifiers
            1..677
            /organism="Pan troglodytes"

```

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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-062016.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          5.0%; Score 86; DB 10; Length 677;
Best Local Similarity 100.0%; Pred.No. 3.6e-32; Indels 0; Gaps 0;
Matches 86; Conservative 0; Mismatches 0;

QY 1244 CTACAGATGAAGAGGGGACCAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTG 1303
DB 301 CTACAGATGAAGAGGGGACCAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTG 360
QY 1304 CCACCTCTGGCTCCTCTGCTGCTTGGC 1329
DB 361 CCCACTCTGGCTCCTCTGCTGCTTGGC 386

RESULT 32
BF191474
LOCUS          537 bp mRNA linear EST 02-NOV-2000
DEFINITION    239074 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION     BF191474
VERSION       BF191474.1 GI:11074843
KEYWORDS      EST.
SOURCE        Sus scrofa (pig)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
              Sus.
REFERENCE     1 (bases 1 to 537)
AUTHORS      Fahrrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
              Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
              Quackenbush,J. and Keele,J.W.
TITLE         Porcine gene discovery by normalized cDNA-library sequencing and
              EST cluster assembly
JOURNAL       Mamm. Genome 13 (8), 475-478 (2002)
PUBMED        12226715
COMMENT       Contact: Smith TPL
              USDA, ARS, US Meat Animal Research Center
              PO Box 166, Clay Center, NE 68933-0166, USA
              Tel: 402 762 4366
              Fax: 402 762 4390
              Email: smith@email.marc.usda.gov
              Single pass sequencing. Bases called and alt trimmed with phred
              v0.980904.e. Vector identified by cross_match with the -minscore 18
              and -minmatch 12 options.
PCR Primers   FORWARD: AGGAACACGCTATGACCAT
              BACKWARD: GTTTCCAGTCACGACG
              Plate: 66 row: F column: 19
              Seq primer: ATTAGGTGACATATAG.
FEATURES      Location/Qualifiers
              1..537
                /organism="Sus scrofa"
                /mol_type="mRNA"
                /db_xref="taxon:9823"
                /tissue_type="pooled"
                /lab_host="DH10B"
                /clone_lib="MARC 2P1G"
                /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
                Library made from pooled tissue from testis, ovary,
                endometrium, hypothalamus, pituitary, and placenta."
ORIGIN
Query Match          3.4%; Score 59; DB 2; Length 537;
Best Local Similarity 100.0%; Pred.No. 2.8e-18; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 0;

QY 790 TCAGACACTGTGTTCTCGGAGAGACCAGTAAGATCTCGGACCTTATCAGCAGCATCAC 848

/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-062016.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          5.0%; Score 86; DB 10; Length 677;
Best Local Similarity 100.0%; Pred.No. 3.6e-32; Indels 0; Gaps 0;
Matches 86; Conservative 0; Mismatches 0;

QY 1244 CTACAGATGAAGAGGGGACCAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTG 1303
DB 301 CTACAGATGAAGAGGGGACCAGGAACCCCTGTGGAGAGGCTTAGACCTGAAGCAGTG 360
QY 1304 CCACCTCTGGCTCCTCTGCTGCTTGGC 1329
DB 361 CCCACTCTGGCTCCTCTGCTGCTTGGC 386

RESULT 33
BG335025
LOCUS          1088 bp mRNA linear EST 27-FEB-2001
DEFINITION    602403470F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541320 5',
              mRNA sequence.
ACCESSION     BG335025
VERSION       BG335025.1 GI:13141463
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
REFERENCE     1 (bases 1 to 1088)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
JOURNAL
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: c9apbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM1219 row: k column: 17
              High quality sequence stop: 556.
              Location/Qualifiers
                1..1088
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:4541320"
                  /tissue_type="choriocarcinoma"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_lib="NIH_MGC_21"
                  /note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
                  Site 2: EcoRI; cDNA made by oligo-dT priming.
                  Directionally cloned into EcoRI/XhoI sites using the
                  following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                  for average insert size 1.8kb. Library constructed by
                  Ling Hong in the laboratory of Gerald M. Rubin (University
                  of California, Berkeley) using ZAP-cDNA synthesis kit
                  (Stratagene) and Superscript II RT (Life Technologies)."
```

AUTHORS Fahrenkrug,S.C., Smith,T.P.L., Preking,B.A., Cho,J., White,J., Vallet,J., Wise,I., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush,J. and Keele,J.W.

TITLE Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly

JOURNAL Mamm. Genome 13 (8), 475-478 (2002)

PUBLISHED 12226715

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAGC
Plate: 30 row: H column: 14
Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers
1. 321
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_hosts="DH10B"
/clone_lib="WARC 2P1G"
/notes="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

FEATURES
source

ORIGIN

Query Match 2.4%; Score 41; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 985 GTCGCCCTCAGCTGCCATGAGACCATGGTGGCTCAGG 1025
|||||
Db 55 GTCGCCCTCAGCTGCCATGAGACCATGGTGGCTCAGG 95
|||||

RESULT 35
LOCUS BY707606
DEFINITION BY707606 RIKEN full-length enriched, 10 day old male pancreas Mus EST. 16-DEC-2002
ACCESSION BY707606
VERSION BY707606.1 GI:27118783
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 1009)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schombach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Sult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawai,H., Kawasawa,Y., Redziarski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,N., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
Location/Qualifiers
1. 1009
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1810019J16"
/sex="male"
/tissue_type="pancreas"
/dev_stage="10 day old"
/clone_lib="RIKEN full-length enriched, 10 day old male pancreas"

ORIGIN

Query Match 2.3%; Score 39; DB 5; Length 1009;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 835 ATCAGCAGCATCATCGCAGGACTACCACTGGATGAGCAG 873
|||||
Db 879 ATCAGCAGCATCATCGCAGGACTACCACTGGATGAGCAG 917
|||||

RESULT 36

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html

Plate: 429 row: E column: 10

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .501

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-429E10"

/sex="Female"

/lab_host="DH10B"

/clone_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 2.2%; Score 38; DB 9; Length 501;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTACCACTGGATGAGCA 872

DB 391 ATCAGCAGCATCAGCAGGACTACCACTGGATGAGCA 354

RESULT 41

BE652359

LOCUS

DEFINITION UI-M-A00-aca-d-03-0-UI.r1 NIH_BMAP.MPG Mus musculus cDNA clone

UI-M-A00-aca-d-03-0-UI 5', mRNA sequence.

ACCESSION BE652359

VERSION BE652359.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

1 (bases 1 to 519)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

889548

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements

FEATURES

source

Seq primer: M13 Reverse.

Location/Qualifiers

1. .519

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-A00-aca-d-03-0-UI"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NIH BMAP MPG"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMAP MPG library is a non-normalized library constructed from mouse pineal gland. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories."

ORIGIN

Query Match 2.2%; Score 38; DB 2; Length 519;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTACCACTGGATGAGCA 872

DB 38 ATCAGCAGCATCAGCAGGACTACCACTGGATGAGCA 75

RESULT 42

BQ566109

LOCUS

DEFINITION

GI52a07.Y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

clone gi52a07 5', mRNA sequence.

ACCESSION BQ566109

VERSION BQ566109.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

1 (bases 1 to 535)

Kachar,B.

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

Unpublished (2002)

Contact: Kachar,B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 52 row: a column: 07

Seq primer: M13RPl reverse primer (ABI).

Location/Qualifiers

1. .535

/organism="Mus musculus"

/mol_type="mRNA"

/strain="BALB/c"

/db_xref="taxon:10090"

/clone="gi52a07"

/sex="male and female"

/dev_stage="Post natal

/clone_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by

cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

ORIGIN

Query Match 2.2%; Score 38; DB 5; Length 535;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTACCACTGGATGAGCA 872

Db 340 ATCAGCAGCATCAGCAGGACTACCACTGGATGAGCA 377

RESULT 43

BG082830

LOCUS BG082830 586 bp mRNA linear EST 18-DEC-2003
DEFINITION H3081C02-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone

ACCESSION BG082830 5', mRNA sequence.

VERSION BG082830.2 GI:40069253

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 586)
Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grabovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H.
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
10922068

TITLE

JOURNAL

PUBMED

COMMENT

On Jan 26, 2001 this sequence version replaced gi:12565398.
Other ESTs: H3081C02-3

Contact: George J. Kargul

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgun.grc.nia.nih.gov

This clone set has been freely distributed to the community. Please

visit <http://lgun.grc.nia.nih.gov/cDNA/15k.html> for details.

Plate: H3081 row: C column: 02

Seq primer: -21M13 Reverse

High quality sequence stop: 586

POLYA=No.

FEATURES

source

Location/Qualifiers

1..586

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="niaEST:H3081C02-5"

/db_xref="taxon:10090"

/clone="H3081C02"

/sex="Clones arrayed from a variety of cDNA libraries"

/dev_stage="Clones arrayed from a variety of cDNA

libraries"

/lab_host="DH10B"

/clone_lib="NIA Mouse 15K cDNA Clone Set"

/notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This

clone is among a rearrayed set of 15,247 clones from 11

embryo cDNA libraries (including preimplantation stage

embryos from unfertilized egg to blastocyst, embryonic

part of E7.5 embryos, extraembryonic part of E7.5

embryos, and E12.5 female mesonephros/gonad) and one

newborn ovary cDNA library. Average insert size 1.5 kb.

All source libraries are cloned unidirectionally with

Oligo(dT)-Not primers. References include: (1)

Genome-wide expression profiling of mid-gestation

placenta and embryo using a 15,000 mouse developmental

cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97:

9127-9132; (2) Large-scale cDNA analysis reveals phased

gene expression patterns during preimplantation mouse

development, 2000, Development, 127: 1737-1749; (3)

Genome-wide mapping of unselected transcripts from

extraembryonic tissue of 7.5-day mouse embryos reveals

enrichment in the t-complex and under-representation on

the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN

Query Match 2.2%; Score 38; DB 2; Length 586;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTACCACTGGATGAGCA 872

Db 99 ATCAGCAGCATCAGCAGGACTACCACTGGATGAGCA 136

RESULT 44

BG657667/c

LOCUS

DEFINITION

musculus cDNA clone D23001M17 5', mRNA sequence.

ACCESSION

VERSION

BB657667 601 bp mRNA linear EST 26-OCT-2001
BB657667 RIKEN full-length enriched, 12 days embryo eyeball Mus

BB657667

GI:16491493

was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

2.2%; Score 38; DB 2; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCACGACGAGTACCACCTGGATGAGCA 872
|||||
Db 519 ATCAGCAGCATCACGACGAGTACCACCTGGATGAGCA 482
|||||

RESULT 45
AG603040/c

LOCUS AG603040 763 bp DNA linear GSS 23-DEC-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-535K05.T7, genomic survey sequence.
ACCESSION AG603040
VERSION AG603040.1 GI:48363870
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and Shiroishi, I.
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PMID 15574823
REFERENCE 2 (bases 1 to 763)
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suhiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: http://bgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center.
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
source 1..763
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-535K05.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match 2.2%; Score 38; DB 10; Length 763;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCACGACGAGTACCACCTGGATGAGCA 872

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Db      462 ATCAGCAGCATCGCAGGACTACCCCTGGATGAGCA 425
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RESULT 46
BI694617
LOCUS   826 bp mRNA linear EST 18-SEP-2001
DEFINITION 603347838F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5375384 5',
mRNA sequence.
ACCESSION BI694617
VERSION   BI694617.1 GI:15657246
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 826)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1955 row: 1 column: 09
High quality sequence stop: 796.

FEATURES
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Location/Qualifiers
1..826
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/strain="FVB/N-3"
/db_xref="taxon:10090"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 2.2%; Score 38; DB 3; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCGCAGGACTACCCCTGGATGAGCA 872
|||||
Db 538 ATCAGCAGCATCGCAGGACTACCCCTGGATGAGCA 575
|||||

RESULT 47
BI694617
LOCUS   918 bp mRNA linear EST 24-OCT-2000
DEFINITION 601787134F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014680 5',
mRNA sequence.
ACCESSION BI694617
VERSION   BI694617.1 GI:10983355
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 918)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Donaldo, Ph.D.
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence start: 28
High quality sequence stop: 840.

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Location/Qualifiers
1..930
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/mol_type="mRNA"

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/clone_lib="NCI CGAP Lu33"
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modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTCAAGTGGAGCGCGCTCTGTGTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

ORIGIN

Query Match 2.2%; Score 38; DB 3; Length 930;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCGAGGACTACCACTGGATGAGCA 872
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 DB 121 ATCAGCAGCATCAGCGAGGACTACCACTGGATGAGCA 158
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RESULT 49
 BF135747
 LOCUS
 DEFINITION 984 bp mRNA linear EST 24-OCT-2000
 60178110F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008914 5',
 mRNA sequence.

ACCESSION BF135747
 VERSION
 KEYWORDS
 SOURCE BF135747.1 GI:10974696
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 984)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM9244 row: d column: 03
 High quality sequence stop: 629.

FEATURES
 source
 1..984
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 /clone="IMAGE:4008914"
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 /lab_host="DH10B"
 /clone_lib="NCI CGAP Lu30"
 /notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; transgenic model WNT-1, expression driven by
 WNTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
 dt. Library constructed by Life Technologies.
 Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 2.2%; Score 38; DB 2; Length 984;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCGAGGACTACCACTGGATGAGCA 872
 |||||||
 DB 237 ATCAGCAGCATCAGCGAGGACTACCACTGGATGAGCA 274
 |||||||

RESULT 50
 AK051860/c
 LOCUS
 DEFINITION 1596 bp mRNA linear HTC 03-APR-2004
 Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length
 enriched library, clone:D230011M17 product:hypothetical protein,
 full insert sequence.

ACCESSION AK051860
 VERSION AK051860.1 GI:26342255
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 10349636

REFERENCE 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 11042159

REFERENCE 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 11076861

REFERENCE 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

REFERENCE 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1596)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers
1. .1596
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:D230011M17"
/db_xref="taxon:10090"
/clone="D230011M17"
/tissue type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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890..1432
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CDS

Query Match 2.2%; Score 38; DB 4; Length 1596;
Best Local Similarity 100.0%; Pred. No. 26-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCAGCAGGACTACCCCTGGATGACGA 872
|||||
Db 519 ATCAGCAGCATCAGCAGGACTACCCCTGGATGACGA 482
|||||

RESULT 51
AK007551
LOCUS
DEFINITION
Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810019J16 product:SIMILAR TO TATA BOX BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE II, C1, 130KD homolog [Mus musculus], full insert sequence.

ACCESSION
AK007551
VERSION
AK007551.1 GI:12841167
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
PUBMED
10349636

REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
PUBMED
11042159

REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hazawa, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okada, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
PUBMED
11076861

REFERENCE
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
REFERENCE
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL
6 (bases 1 to 1657)
AUTHORS
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirakawa, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saio, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, K., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamatsu, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
TITLE
Direct Submission
JOURNAL
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT
Please visit our web site (http://genome.gsc.riken.jp/) for further details.

FEATURES
source
1. .1657
/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="FANTOM DB:1810019J16"
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/clone="1810019J16"
/sex="male"
/tissue type="pancreas"
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/dev_stage="10 day old"
138..1241
/note="unnamed protein product; SIMILAR TO TATA BOX

CDS

BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA POLYMERASE II, Cl. 130KD homolog [Mus musculus] (SPTR|Q92200, evidence: PASTY, 97.2%ID, 100%length, match=649) putative"

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GVPPSPDRPPRRDQQRUKTSGSGSFSPDVVKLGIPVYPRHATSPVPDVSCKKE
PLAEPPTTHSLPSTDTNPMGSEYYSPHESDLDPENMGSGMSRSLIDVLIFKKLT
ELFVHQIDELAKTSDTVFLKTSKISDLISITQDYHLDEQDAEGRLVGIRIST
RKSRRSPQTSKGRAPASAPSGSGHETMGLSGLSQDELTVQISQETTAIAARKL
RYPGAPGYPASQSSFGQDTDDSSGAPLLQVVC"

ORIGIN

Query Match 2.2%; Score 38; DB 4; Length 1657;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 ATCAGCAGCATCCGCGAGCACTACCACTCGGTGATGACA 872
|||||
DB 882 ATCAGCAGCATCCGCGAGCACTACCACTCGGTGATGACA 919
|||||

RESULT 52

LOCUS AI669760/c
DEFINITION tui2h08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2250879 3',
mRNA sequence.

ACCESSION AI669760

VERSION 1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 488)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 792 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 452.

FEATURES

source

1. .488
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2250879"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr28"
/notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker: Plasmid DNA from the
normalized library NCI CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonesIDs

ORIGIN

Query Match 2.2%; Score 37; DB 1; Length 488;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1402 TGATCCCTGCCAGGCCCTTCCTTCCTGCTCATGCT 1438
|||||
DB 352 TGATCCCTGCCAGGCCCTTCCTTCCTGCTCATGCT 316
|||||

RESULT 53

BP111348

LOCUS

DEFINITION BP111348 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone
ORCS11684 5', mRNA sequence.

ACCESSION BP111348

VERSION

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Gozoh Tsujimoto

Department of Molecular, Cell Pharmacology

National Research Institute for Child Health and Development

3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan

Tel: 81-3-3149-2476

Fax: 81-3-3149-1252

Email: gtsujimoto@nch.go.jp

This work was performed to collaborate with Developmental Biology

Department, National Institute of Agrobiological Sciences. Address:

2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:

81-29-838-8633 e-mail: kazuh@aaffrc.go.jp

This work was funded by Organized Research Combination System

(ORCS) project of Ministry of Education, Culture, Sports, Science

and Technology.

Location/Qualifiers

1. .605

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/clone="ORCS11684"

/tissue_type="mixture of uterus and placenta"

/dev_stage="adult"

/clone_lib="ORCS bovine utero-placenta cDNA"

ORIGIN

Query Match 2.0%; Score 35; DB 3; Length 605;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 877 GCTGAGGCGCGCTGTGTCACGCGGCATTCGCAT 911
|||||

DB 57 GCTGAGGCGCGCTGTGTCACGCGGCATTCGCAT 91
|||||

RESULT 54

LOCUS

DEFINITION

ACCESSION

CB463434

CB463434

CB463434

CB463434

CB463434

CB463434

CB463434

```

VERSION      CB463434.1  GI:29269819
KEYWORDS     EST.
SOURCE       Bos taurus (cow)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
             Pecora; Bovidae; Bovinae; Bos.
REFERENCE    1 (bases 1 to 585)
AUTHORS      Smith,T.P.L., Roberts,A.J., Echterkamp,S.E., Chitko-McKown,C.G.,
             Wray,J.E. and Keele,J.W.
TITLE        A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL      Unpublished (2003)
COMMENT      Contact: Smith TPL
             USDA, ARS, US Meat Animal Research Center
             PO Box 166, Clay Center, NE 68933-0166, USA
             Tel: 402 762 4366
             Fax: 402 762 4390
             Email: smith@mail.marc.usda.gov
             Single pass sequencing. Bases called with phred v0.020425.c and
             trimmed with the aid of the trim_alt option. Vector identified with
             cross_match v0.990329.
             Plate: LAM8004 row: M column: 8
             Seq primer: GTAATACGACTCACTATAGG.
FEATURES     Location/Qualifiers
             source          1..585
                        /organism="Bos taurus"
                        /mol_type="mRNA"
                        /db_xref="taxon:9913"
                        /tissue_type="pooled"
                        /lab_host="DH108"
                        /clone_lib="MARC 6BOV"
                        /notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
                        Library made with RNA pooled from multiple tissues
                        including liver, lung, hypothalamus, pituitary, and
                        placenta/endometrium."
ORIGIN
Query Match      1.9%; Score 32; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 GACTCATCTTCAGGCGCAGCAGACGACTC 1163
      |||||||
Db 134 GACTCATCTTCAGGCGCAGCAGACGACTC 165

RESULT 55
CW991025/c
LOCUS          260 bp mRNA linear GSS 20-JUL-2005
DEFINITION    BC0173 Sanger Institute Gene Trap Library pG72lrx Mus musculus
               cDNA, mRNA sequence.
ACCESSION     CW991025
VERSION       CW991025.3 GI:62470582
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
             Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 260)
AUTHORS       Sanger Institute Gene Trap Resource - SIGTR.
TITLE         http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL       Unpublished (2003)
COMMENT       On Feb 25, 2005 this sequence version replaced gi:60285534.
             Wellcome Trust Sanger Institute
             Email: info.genetrap@sanger.ac.uk
             Sequence tag generated by 5' RACE of total RNA from gene trap ES
             cell line. ES cell lines harboring insertion mutation of target
             gene are available upon request from Sanger Institute Gene Trap
             Resource. Annotation information available from
             http://www.sanger.ac.uk/PostGenomics/genetrap/
             Class: Gene Trap.

```

```

FEATURES     Location/Qualifiers
             source          1..260
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="129 OLA"
                        /db_xref="taxon:10090"
                        /sex="Male"
                        /cell_type="Embryonic Stem Cell"
                        /clone_lib="Sanger Institute Gene Trap Library pG72lrx"
                        /notes="Vector: pGT2lrx"
ORIGIN
Query Match      1.7%; Score 29; DB 10; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 TTCAAGAAGCTGACAGAGCTGTTTCAGCGT 758
      |||||||
Db 208 TTCAAGAAGCTGACAGAGCTGTTTCAGCGT 180

RESULT 56
CB759331
LOCUS          434 bp mRNA linear EST 16-MAY-2003
DEFINITION    AMGNNUC:NRPI4-00055-F9-A W Rat pituitary (10472) Rattus norvegicus
               cDNA clone nrpi4-00055-f9 5', mRNA sequence.
ACCESSION     CB759331
VERSION       CB759331.1 GI:29847722
KEYWORDS      EST.
SOURCE        Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
             Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
             Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE     1 (bases 1 to 434)
AUTHORS       Angen EST Program.
TITLE         Angen Rat EST Program
JOURNAL       Unpublished (2003)
COMMENT       Contact: Dan Fitzpatrick
             Angen, Inc
             One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
             Tel: 805 447-4881
             Plate: 00055 row: f column: 9.
FEATURES     Location/Qualifiers
             source          1..434
                        /organism="Rattus norvegicus"
                        /mol_type="mRNA"
                        /db_xref="taxon:10116"
                        /clone_lib="W Rat pituitary (10472)"
                        /notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat
                        pituitary adult female Wistar rat avg insert size 2.1 kb"
ORIGIN
Query Match      1.7%; Score 29; DB 6; Length 434;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 GACAGTGGCCATGACAGACCATGTGGGCTC 1022
      |||||||
Db 76 GACAGTGGCCATGACAGACCATGTGGGCTC 104

RESULT 57
BE533148
LOCUS          609 bp mRNA linear EST 09-AUG-2000
DEFINITION    601235445F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3599314 5',
               mRNA sequence.
ACCESSION     BE533148
VERSION       BE533148.1 GI:9761793
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 609)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM8781 row: i column: 11
High quality sequence stop: 587.

FEATURES
source

1. 609
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mrna"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:359314"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 1.7%; Score 29; DB 2; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.008; 0; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 0;

QY 142 AAGGACCTGGCCACCATGGCCAGAG 170
Db 172 AAGGACCTGGCCACCATGGCCAGAG 200

RESULT 58
BI078885
LOCUS
DEFINITION

BI078885 602873115F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5005226 5',
mRNA sequence.

ACCESSION BI078885
VERSION 1
KEYWORDS GI:14497215
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 738)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11044 row: m column: 03
High quality sequence stop: 735.

FEATURES
source

Location/Qualifiers
1. 738
/organism="Mus musculus"
/mol_type="mrna"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5005226"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 1.7%; Score 29; DB 2; Length 738;
Best Local Similarity 100.0%; Pred. No. 0.0082; 0; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 0;

QY 142 AAGGACCTGGCCACCATGGCCAGAG 170
Db 375 AAGGACCTGGCCACCATGGCCAGAG 403

RESULT 59
BG871324
LOCUS

DEFINITION BG871324 602792482F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923597 5',
mRNA sequence.

ACCESSION BG871324
VERSION 1
KEYWORDS GI:14221864
SOURCE EST.
ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10845 row: c column: 22
High quality sequence start: 114
High quality sequence stop: 750.

FEATURES
source

Location/Qualifiers
1. 756
/organism="Mus musculus"
/mol_type="mrna"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4923597"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_SG2"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 1.7%; Score 29; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.0082; 0; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 0;

Qy 142 AAGACCTGGCCACCATGGCCAGAG 170
 Db 216 AAGACCTGGCCACCATGGCCAGAG 244

RESULT 60
 BF041373
 LOCUS
 DEFINITION BF041373 485 bp mRNA linear EST 10-OCT-2000
 clone BP250025B20B12 5', mRNA sequence.

ACCESSION
 VERSION BF041373
 KEYWORDS
 SOURCE EST.
 ORGANISM Bos taurus (cow)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 485)

TITLE
 JOURNAL
 COMMENT Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and
 Larson, J.H.
 Bovine ESTs
 Unpublished (2000)
 Contact: Lewin, H. A.
 W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National
 Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
 from Washington University Genome Center. Vector Trimmi g:
 Cross_match from Washington University Genome Center PHRAP suite.
 This sequence is vector free and at least 200 bp in length.

PCR Primers
 FORWARD: TAATACGACTCACTATAGG
 BACKWARD: ATTAACCTCTCACTAAG
 Insert Length: 485 Std Error: 0.00
 Plate: BP250025B20 row: B column: 12
 Seq primer: AGCGATACAAATTCACAGGA
 High quality sequence stop: 485.

FEATURES
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 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="BP250025B20B12"
 /sex="female"
 /lab_host="DH10B"
 /note="Organ: placenta; Vector: pT73Pac; Site 1: EcoRI;
 Site 2: NotI; The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6(9): 791-806."

ORIGIN
 Query Match 1.6%; Score 28; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 CCTGCTGCTGCTGCTGCGACCTGGGT 245
 Db 278 CCGTCTGCTGCTGCTGCGACCTGGGT 305

RESULT 61
 AL724130/c
 LOCUS
 DEFINITION AL724130 547 bp mRNA linear EST 18-APR-2002

DEFINITION AL724130 Danio rerio embryonic inner ear subtracted cDNA Danio
 rerio cDNA clone BN0AA073ZB04 5', mRNA sequence.

ACCESSION
 VERSION AL724130
 KEYWORDS
 SOURCE EST.
 ORGANISM Danio rerio (zebrafish)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 547)

TITLE
 JOURNAL
 COMMENT Coimbra, R., Weil, D., Bottier, P., Blanchard, S., Levi, M.,
 Hardelin, J.P., Weissenbach, J. and Petit, C.
 A subtracted cDNA library from the zebrafish (Danio rerio)
 embryonic inner ear
 Unpublished (2002)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 1..547
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="BN0AA073ZB04"
 /tissue_type="inner ear"
 /dev_stage="embryonic"
 /clone_lib="Danio rerio embryonic inner ear subtracted
 cDNA"
 /note="subtracted cDNA library"

ORIGIN
 Query Match 1.6%; Score 28; DB 1; Length 547;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1686 TTTGTAGTACCTCGCGCGACCGC 1713
 Db 31 TTTGTAGTACCTCGCGCGACCGC 4

RESULT 62
 AL730744/c
 LOCUS
 DEFINITION AL730744 629 bp mRNA linear EST 18-APR-2002
 rerio cDNA clone BN0AA116ZH12 5', mRNA sequence.

ACCESSION
 VERSION AL730744
 KEYWORDS
 SOURCE EST.
 ORGANISM Danio rerio (zebrafish)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 629)

TITLE
 JOURNAL
 COMMENT Coimbra, R., Weil, D., Bottier, P., Blanchard, S., Levi, M.,
 Hardelin, J.P., Weissenbach, J. and Petit, C.
 A subtracted cDNA library from the zebrafish (Danio rerio)
 embryonic inner ear
 Unpublished (2002)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 1..629
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="BN0AA116ZH12"
 /tissue_type="inner ear"
 /dev_stage="embryonic"


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/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match      1.6%; Score 28; DB 1; Length 629;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 TTGTGAAGTACCTCGCGCGGACACGC 1713
Db 31 TTGTGAAGTACCTCGCGCGGACACGC 4

RESULT 63
AL715958/c
LOCUS AL715958 765 bp mRNA linear EST 18-APR-2002
DEFINITION AL715958 Danio rerio embryonic inner ear subtracted cDNA Danio
            rerio cDNA clone BN0AA011ZE08 3', mRNA sequence.
ACCESSION AL715958
VERSION AL715958.1 GI:20180561
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 765)
AUTHORS Coimbra.R., Well.D., Brottier.P., Blanchard.S., Levi.M.,
            Hardelin,J.P., Weissbach,J. and Petit,C.
TITLE A subtracted cDNA library from the zebrafish (Danio rerio)
JOURNAL Unpublished (2002)
COMMENT Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES             source
source 1..765
            /organism="Danio rerio"
            /mol_type="mRNA"
            /db_xref="taxon:7955"
            /clone="BN0AA011ZE08"
            /tissue_type="inner ear"
            /dev_stage="embryonic"
            /clone_lib="Danio rerio embryonic inner ear subtracted
            cDNA"
            /note="subtracted cDNA library"

ORIGIN
Query Match      1.6%; Score 28; DB 1; Length 765;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 TTGTGAAGTACCTCGCGCGGACACGC 1713
Db 29 TTGTGAAGTACCTCGCGCGGACACGC 2

RESULT 64
CA736276
LOCUS CA736276 369 bp mRNA linear EST 26-NOV-2002
DEFINITION wpils.pk007.a7 wpils Triticum aestivum cDNA clone wpils.pk007.a7 5'
            end, mRNA sequence.
ACCESSION CA736276
VERSION CA736276.1 GI:25551874
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 369)

```

```

Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
            Location/Qualifiers
            1..369
            /organism="Triticum aestivum"
            /mol_type="mRNA"
            /db_xref="taxon:4565"
            /clone="wpils.pk007.a7"
            /tissue_type="leaf"
            /lab_host="DH10B"
            /clone_lib="wpils"
            /note="Vector: PGEM-T Easy; Site 1: SmaI; Wheat, Polk
            cultivar (resistant), infected with septoria tritici
            strain A 24 hours after infection"

ORIGIN
Query Match      1.6%; Score 27; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TTGTGAAGTACCTCGCGCGGACACGC 1713
Db 341 TTGTGAAGTACCTCGCGCGGACACGC 367

RESULT 65
AI267255/c
LOCUS AI267255 535 bp mRNA linear EST 17-NOV-1998
DEFINITION aq62h05.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone
            IMAGE:2035545, mRNA sequence.
ACCESSION AI267255
VERSION AI267255.1 GI:3886422
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1 (bases 1 to 535)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
            WashU-NCI human EST Project
            Unpublished (1997)
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -400P from Gibco
            High quality sequence stop: 442.
            Location/Qualifiers
            1..535
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2035545"
            /tissue_type="frontal lobe (see description)"
            /lab_host="DH10B (phage-resistant)"

```

/clone_lib=Stanley Frontal SN pool 2"
 /notes=Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
 Site 1: EcoRI; Total RNA (purified with Trizol and DNaseI
 before use) was reverse transcribed using a modified
 oligo-dT primer containing Real and HindIII sites.
 Double-stranded cDNA was digested with Real, resulting in
 blunt ended cDNA of an average 0.1-2 kb in length.
 Digested cDNA was split into two sets, one used as is as
 the driver, the other set was split in half again and each
 half linked to a different adaptor
 (5'-TCGAGCGCGCGCGGAGGT-3' or 5'-
 AGGCGTGTGCGGAGGCGGT-3'), to be used as tester.
 Subtraction was performed using the Clontech PCR Select
 cDNA subtraction kit. Pool of two schizoprenics, male age
 44 and female age 56 (S-116, S-118) subtracted by pool of
 two mentally normal male individuals ages 41 and 53
 (S-124, S-141). Tissues were obtained from the Stanley
 Neuropathology Consortium (www.stanleylab.org). Library
 constructed and subtracted by Dr. Nancy Johnston [(410)
 614-3918, nlj@welchlink.welch.jhu.edu]."

ORIGIN

Query Match 1.6%; Score 27; DB 1; Length 535;
 Best Local Similarity 100.0%; Pred. No. 0.085;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TTGTAACTACCTCGCGGCGGACACGC 1713

Db 27 TTGTAACTACCTCGCGGCGGACACGC 1

RESULT 66

LOCUS CB457332 600 bp mRNA linear EST 26-MAR-2003
 DEFINITION 714674 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION CB457332
 VERSION CB457332.1 GI:29263714
 KEYWORDS EST.
 SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 600)
 Smith, T.P.L., Roberts, A.J., Echterkamp, S.E., Chitko-McKown, C.G.,
 Wray, J.E. and Keefe, J.W.
 A second set of bovine ESTs from pooled-tissue normalized libraries
 Unpublished (2003)
 Contact: Smith TPL

TITLE

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_call option. Vector identified with
 cross match v0.990329.

Plate: FQY8071 row: A column: 24

Seq primer: GTAATACGACTCATATAGG.

FEATURES

Location/Qualifiers

1..600

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH108"

/clone_lib="MARC 6BOV"

/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 Library made with RNA pooled from multiple tissues
 including liver, lung, hypothalamus, pituitary, and
 placenta/endometrium."

ORIGIN

Query Match 1.6%; Score 27; DB 6; Length 600;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 GACTCATCTTCAGGCGGACGACACA 1158

Db 133 GACTCATCTTCAGGCGGACGACACA 159

RESULT 67

LOCUS AL718806/c 609 bp mRNA linear EST 18-APR-2002
 DEFINITION AL718806 Danio rerio embryonic inner ear subtracted cDNA Danio
 rerio cDNA clone BN0AA037ZE05 3', mRNA sequence.

ACCESSION AL718806

VERSION AL718806.1 GI:20183410

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 609)

Coimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M.,

Hardelin, J.P., Weissenbach, J. and Petit, C.

A subtracted cDNA library from the zebrafish (Danio rerio)

embryonic inner ear

Unpublished (2002)

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..609

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="BN0AA037ZE05"

/tissue_type="inner ear"

/dev_stage="embryonic"

/clone_lib="Danio rerio embryonic inner ear subtracted

cDNA"

/note="subtracted cDNA library"

ORIGIN

Query Match 1.6%; Score 27; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 TTTGTAAGTACCTCGCGGCGGACG 1712

Db 48 TTTGTAAGTACCTCGCGGCGGACG 22

RESULT 68

LOCUS CX067711/c 733 bp mRNA linear EST 03-JAN-2005
 DEFINITION 1322352 NCCWA 04RT Oncorhynchus mykiss cDNA, mRNA sequence.
 ACCESSION CX067711

VERSION CX067711.1 GI:56989277

KEYWORDS EST.

SOURCE Oncorhynchus mykiss (rainbow trout)

ORGANISM

Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 733)

Rexroad, C.E., Rise, M., Koop, B., von Schalburg, K. and Yao, J.

04RT grool, NCCWA/WVU EST Project, Phase II, in collaboration with

GRASP

Unpublished (2004)

Contact: Rexroad CE

USDA, ARS, National Center for Cool and Cold Water Aquaculture

11876 Leetown Road, Kearneysville, WV 25430, USA

Tel: 304 724 8340 x2129

Fax: 304 725 0351

Email: crexroad@cccwa.ars.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the alt option. Vector identified with cross_match v0.990329.

Plate: 106 row: I column: 19

Seq primer: GTAAATACGACTCACTATAGG.

Location/Qualifiers

1..733

/organism="Onchornynchus mykiss"

/mol_type="mRNA"

/db_xref="taxon:8022"

/lab_host="Top10"

/clone_lib="NCCCWA 04RT"

/note="Vector: PCR 4-TOPO; This is an early neurogenesis SSH library created by Mathew L. Rise constructed by subtracting late neurogenesis (mixed stages: hindbrain swelling + heart tube with peristalsis) from early neurogenesis (mixed stages: neural groove + 1/2 epiboly). Fish were from a domesticated strain (Spring Valley Trout Farm, Langley, B.C.), courtesy of Bob Devlin, DFO. These are mostly internal (coding) sequences."

ORIGIN

Query Match 1.6%; Score 27; DB 8; Length 733;

Best Local Similarity 100.0%; Pred. No. 0.088;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TTGTAAGTACCTCGGCGGACACGC 1713

DB 33 TTGTAAGTACCTCGGCGGACACGC 7

RESULT 69

AL717228/c

LOCUS

DEFINITION AL717228 Danio rerio embryonic inner ear subtracted cDNA Danio

rerio cDNA clone BN0AA025ZB11 3', mRNA sequence.

AL717228

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 738)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..738

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="BN0AA025ZB11"

/tissue_type="inner ear"

/dev_stage="embryonic"

/clone_lib="Danio rerio embryonic inner ear subtracted

cDNA"

/note="subtracted cDNA library"

ORIGIN

Query Match

Best Local Similarity 1.6%; Score 27; DB 1; Length 738;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TTGTAAGTACCTCGGCGGACACGC 1713

DB 30 TTGTAAGTACCTCGGCGGACACGC 4

RESULT 70

DN615123/c

LOCUS

DEFINITION

DN615123

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

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comparable uninfected leaves"

ORIGIN
Query Match          1.5%; Score 26; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGCGCGGACACACGC 1713
      |||||
Db 205 TGTAACTACTCGCGCGGACACACGC 230

RESULT 74
AL726074/c
LOCUS
DEFINITION AL726074 Danio rerio embryonic inner ear subtracted cDNA Danio
reio cDNA clone BN0AA080ZD03 5', mRNA sequence.
ACCESSION AL726074
VERSION AL726074.1 GI:20190678
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 255)
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
Hardelin,J.P., Weissenbach,J. and Petit,C.
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Unpublished (2002)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .255
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA080ZD03"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match          1.5%; Score 26; DB 1; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGCGCGGACACACGC 1713
      |||||
Db 29 TGTAACTACTCGCGCGGACACACGC 4

RESULT 75
AI267488/c
LOCUS
DEFINITION AI267488 288 bp mRNA linear EST 17-NOV-1998
IMAGE:2035800, mRNA sequence.
ACCESSION AI267488
VERSION AI267488.1 GI:3886655
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 288)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,P.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 287.
Location/Qualifiers
1. .288
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2035800"
/tissue_type="frontal lobe (see description)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Stanley Frontal SN pool 2"
/note="Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
Site 1: EcoRI; Total RNA (purified with Trizol and DNaseI
before use) was reverse transcribed using a modified
oligo-dT primer containing RsaI and HindIII sites.
Double- stranded cDNA was digested with RsaI, resulting in
blunt ended cDNA of an average 0.1-2 kb in length.
Digested cDNA was split into two sets, one used as is as
the driver, the other set was split in half again and each
half linked to a different adaptor
(5'-TCGAGCGCGCGCGGCGGAGT-3' or 5'-
AGCGGTGTCGCGGAGCGGCGT-3'), to be used as tester.
Subtraction was performed using the Clontech PCR Select
cDNA subtraction kit. Pool of two schizoprenics, male age
44 and female age 56 (S-116, S-118) subtracted by pool of
two mentally normal male individuals ages 41 and 53
(S-124, S-141). Tissues were obtained from the Stanley
Neuropathology Consortium (www.stanleylab.org). Library
constructed and subtracted by Dr. Nancy Johnston [(410)
614-3918, nlj@weilchlink.weilch.jhu.edu]."
```

E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.

FEATURES

Location/Qualifiers
1..344
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wpils.pk002.e11"
/issue_type="leaf"
/lab_host="DH10B"
/clone_lib="wpils"

/note="Vector: pGEM-T Easy; Site 1: SmaI; Wheat, Polk cultivar (resistant), infected with septoria tritici strain A 24 hours after infection"

ORIGIN

Query Match 1.5%; Score 26; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACCTCGCGCGACCGC 1713

Db 28 TGTAACTACCTCGCGCGACCGC 3

RESULT 77

AW481164
LOCUS
DEFINITION 34685 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION
VERSION AW481164.1 GI:7051270
KEYWORDS
SOURCE Bos taurus (cow)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS
1 (bases 1 to 402)
Smith,T.P.L., Grosse,W.M., Preking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A.,
Chitko-McKown,C.G., Perlea,G., Holt,I., Karamecheva,S., Liang,F.,
Quackenbush,J. and Keese,J.W.

TITLE
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

JOURNAL

PUBMED

COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 20

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCCGAGTCACGACG

Plate: 18 row: G column: 24

Seq primer: ATTAGTGACACTATAG.

FEATURES

Location/Qualifiers
1..402
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/issue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 1BOV"

ORIGIN

Query Match 1.5%; Score 26; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1295 GAAGCAGTGCCCACTCTGGCTCTCC 1320

Db 68 GAAGCAGTGCCCACTCTGGCTCTCC 93

RESULT 78

BF150866
LOCUS
DEFINITION BF150866.1 GI:11032261
425 bp mRNA linear EST 29-DEC-2000
uy88g10.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666690 5',
mRNA sequence.

ACCESSION

VERSION BF150866.1 GI:11032261

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 425)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Other ESTs: uy88g10.x1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

image.lnl.gov/image/html/iresources.shtml

MGI:1427458

Seq primer: -40RP from Gibco

High quality sequence stop: 395.

FEATURES

source

1..425

/organism="Mus musculus"

/mol_type="mRNA"

/strain="mix FVB/N, C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:3666690"

/issue_type="tumor, gross tissue"

/dev_stage="7 months"

/lab_host="DH10B"

/clone_lib="NCI CGAP Mam5"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Robin Humphreys,

NIH"

ORIGIN

Query Match 1.5%; Score 26; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 GGGCTGCTTCTGCTTCGCGCGCTGC 285

Db 81 GGGCTGCTTCTGCTTCGCGCGCTGC 106

RESULT 79
AW762557
LOCUS
DEFINITION
426 bp mRNA linear EST 04-MAY-2000
ur57f12.y1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3154415 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Murinae; Mus.
REFERENCE
1 (bases 1 to 426)
AUTHORS
TITLE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other ESTs: ur57f12.x1
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1057171
Seq primer: -4ORP from Gibco
High quality sequence stop: 422.
FEATURES
source
1. .426
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129, C57BL/6J, FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3154415"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 487 GATGTTAAGCTCAAGGCATCCCTGT 512
Db 227 GATGTTAAGCTCAAGGCATCCCTGT 252
RESULT 80
CB732455
LOCUS
DEFINITION
475 bp mRNA linear EST 11-APR-2003
AMGNNUC:SRCS1-00007-E10-A srcs1 (10883) Rattus norvegicus cDNA
clone srcs1-00007-e10 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Murinae; Rattus.
REFERENCE
1 (bases 1 to 475)
AUTHORS
TITLE
Angen EST Program.
Angen Rat EST Program
Unpublished (2003)
COMMENT
Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00007 row: e column: 10.
FEATURES
source
1. .475
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="srcs1-00007-e10"
/tissue_type="Cornea"
/clone_lib="srcs1 (10883)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Site_2: EcoRI;
rat corneas"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 475;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAACTACTCGCGCGGACCAACGC 1713
Db 450 TGTAACTACTCGCGCGGACCAACGC 475
RESULT 81
CA882810/c
LOCUS
DEFINITION
485 bp mRNA linear EST 20-DEC-2002
SSH160 Rice callus and differential tissue SSH library Oryza
sativa cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 485)
AUTHORS
TITLE
Rice cDNA from callus (2002)
JOURNAL
COMMENT
Contact: DU Xiling
Institute of Genetics, Fudan University
Handan Road 220, Shanghai 200433, China
Tel: 86-21-6564-3715
Email: dxiling@yahoo.com.cn.
FEATURES
source
1. .485
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Wuyunjing No. 7"
/db_xref="taxon:4530"
/clone_lib="Rice callus and differential tissue SSH
library"
/note="Vector: pGEM-T; suppressed subtract hybridized
cDNA prepared from rice callus mRNAs
ligating to
pGEM-T"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAACTACTCGCGCGGACCAACGC 1713
Db 81 TGTAACTACTCGCGCGGACCAACGC 56

REFERENCE
1 (bases 1 to 475)
AUTHORS
TITLE
JOURNAL
COMMENT
Angen EST Program.
Angen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00007 row: e column: 10.
FEATURES
source
1. .475
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="srcs1-00007-e10"
/tissue_type="Cornea"
/clone_lib="srcs1 (10883)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Site_2: EcoRI;
rat corneas"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 475;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAACTACTCGCGCGGACCAACGC 1713
Db 450 TGTAACTACTCGCGCGGACCAACGC 475
RESULT 81
CA882810/c
LOCUS
DEFINITION
485 bp mRNA linear EST 20-DEC-2002
SSH160 Rice callus and differential tissue SSH library Oryza
sativa cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 485)
AUTHORS
TITLE
Rice cDNA from callus (2002)
JOURNAL
COMMENT
Contact: DU Xiling
Institute of Genetics, Fudan University
Handan Road 220, Shanghai 200433, China
Tel: 86-21-6564-3715
Email: dxiling@yahoo.com.cn.
FEATURES
source
1. .485
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Wuyunjing No. 7"
/db_xref="taxon:4530"
/clone_lib="Rice callus and differential tissue SSH
library"
/note="Vector: pGEM-T; suppressed subtract hybridized
cDNA prepared from rice callus mRNAs
ligating to
pGEM-T"
ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1688 TGTAACTACTCGCGCGGACCAACGC 1713
Db 81 TGTAACTACTCGCGCGGACCAACGC 56

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RESULT 82
CF036397/c
LOCUS
DEFINITION QCG30h07.yg QCG Zea mays cDNA clone QCG30h07, mRNA sequence. EST 17-JUL-2003
ACCESSION CF036397
VERSION CF036397.1 GI:32931585
KEYWORDS
SOURCE
ORGANISM Zea mays
            501 bp mRNA linear EST 17-JUL-2003
            cDNA clone QCG30h07, mRNA sequence.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.

FEATURES
source
    1..501
    /organism="Zea mays"
    /mol_type="mRNA"
    /cultivar="P2"
    /db_xref="taxon:4577"
    /clone="QCG30h07"
    /tissue_type="embryo"
    /clone_lib="QCG"

ORIGIN
Query Match 1.5%; Score 26; DB 6; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACCTCGCGCGGACCGC 1713
|||||
DB 28 TGTAACTACCTCGCGCGGACCGC 3

RESULT 83
AL720496/c
LOCUS
DEFINITION AL720496 Danio rerio embryonic inner ear subtracted cDNA Danio
            520 bp mRNA linear EST 18-APR-2002
            rero cDNA clone BN0AA0482B03 3', mRNA sequence.
ACCESSION AL720496
VERSION AL720496.1 GI:20185100
KEYWORDS
SOURCE
ORGANISM Danio rerio (zebrafish)
            520 bp mRNA linear EST 18-APR-2002
            rero cDNA clone BN0AA0482B03 3', mRNA sequence.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
            Location/Qualifiers
FEATURES
source
    1..520
    /organism="Danio rerio"
    /mol_type="mRNA"
    /db_xref="taxon:7955"

/clone="BN0AA0482B03"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"
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ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACCTCGCGCGGACCGC 1713
|||||
DB 29 TGTAACTACCTCGCGCGGACCGC 4

RESULT 84
AI267373/c
LOCUS
DEFINITION aiq64C09.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone
            543 bp mRNA linear EST 17-NOV-1998
            IMAGE:2035696, mRNA sequence.
ACCESSION AI267373
VERSION AI267373.1 GI:3886540
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
            543 bp mRNA linear EST 17-NOV-1998
            aiq64C09.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone
            IMAGE:2035696, mRNA sequence.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 437.
            Location/Qualifiers
FEATURES
source
    1..543
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:2035696"
    /tissue_type="frontal lobe (see description)"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="Stanley Frontal SN pool 2"
    /note="Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
    Site 1: EcoRI; Total RNA (purified with Trizol and DNaseI
    before use) was reverse transcribed using a modified
    oligo-dT primer containing Real and HindIII sites.
    Double- stranded cDNA was digested with Real, resulting in
    blunt ended cDNA of an average 0.1-2 kb in length.
    Digested cDNA was split into two sets, one used as is as
    the driver, the other set was split in half again and each
    half linked to a different adaptor
    (5'-TCGAGCGCGCGCGGCGGT-3', or 5'-
    AGGCGTGTGCGGAGCGGT-3'), to be used as tester.
    Subtraction was performed using the Clontech PCR Select
    cDNA subtraction kit. Pool of two schizophrenics, male age
    44 and female age 56 (S-116, S-118) subtracted by pool of
    two mentally normal male individuals ages 41 and 53
    (S-124, S-141). Tissues were obtained from the Stanley
    Neuropathology Consortium (www.stanleylab.org). Library
```



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constructed and subtracted by Dr. Nancy Johnston [(410)
614-3918, nlj@welchlink.welch.jhu.edu]."
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ORIGIN

Query Match 1.5%; Score 26; DB 1; Length 543;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGCGCGGACACCGC 1713
|||||
DB 26 TGTAACTACTCGCGCGGACACCGC 1

RESULT 85
CB464871/C

LOCUS 726118 MARC 6BOV Bos taurus cDNA 3', mRNA linear EST 26-MAR-2003
DEFINITION CB464871
ACCESSION
VERSION CB464871.1 GI:29271256
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 547)
Smith, P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G.,
Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: LAM8004 row: M column: 8
Seq primer: TAGAGCGACAGTCGAGG.
Location/Qualifiers
1. .547
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN

Query Match 1.5%; Score 26; DB 6; Length 547;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1295 GAAGCAGTGCCTCTGGCTCTCC 1320
|||||
DB 474 GAAGCAGTGCCTCTGGCTCTCC 449

RESULT 86
AL714240/C

LOCUS AL714240
DEFINITION AL714240 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone BN0AA003ZC08 5', mRNA sequence.
ACCESSION AL714240
VERSION
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 557)
Coimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M.,
Hardelin, J.P., Weissenbach, J. and Petit, C.
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Unpublished (2002)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .557
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA003ZC08"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN

Query Match 1.5%; Score 26; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGCGCGGACACCGC 1713
|||||
DB 29 TGTAACTACTCGCGCGGACACCGC 4

RESULT 87
AL714414

LOCUS AL714414
DEFINITION AL714414 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone BN0AA005ZH12 5', mRNA sequence.
ACCESSION AL714414
VERSION
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 557)
Coimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M.,
Hardelin, J.P., Weissenbach, J. and Petit, C.
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Unpublished (2002)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .557
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA005ZH12"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN

Query Match 1.5%; Score 26; DB 1; Length 557;

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Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;

QY 1688 TGTAAAGTACCTCGCGCGGACACGC 1713
Db 531 TGTAAAGTACCTCGCGCGGACACGC 556

RESULT 88
AL714437/c
LOCUS
DEFINITION
AL714437 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone EN0AA005ZH12 3', mRNA sequence.
ACCESSION
AL714437
VERSION
AL714437.1 GI:20179040
KEYWORDS
EST.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 558)
AUTHORS
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
Hardelin,J.P., Weissenbach,J. and Petit,C.
TITLE
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
JOURNAL
Unpublished (2002)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1.558
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="EN0AA005ZH12"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 558;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Indels 0; Gaps 0;

QY 1688 TGTAAAGTACCTCGCGCGGACACGC 1713
Db 29 TGTAAAGTACCTCGCGCGGACACGC 4

RESULT 89
AL714276/c
LOCUS
DEFINITION
AL714276 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone EN0AA003ZC08 3', mRNA sequence.
ACCESSION
AL714276
VERSION
AL714276.1 GI:20178879
KEYWORDS
EST.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 561)
AUTHORS
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
Hardelin,J.P., Weissenbach,J. and Petit,C.
TITLE
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
JOURNAL
Unpublished (2002)
COMMENT
Contact: Genoscope
```

```
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1.561
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA003ZC08"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAAGTACCTCGCGCGGACACGC 1713
Db 533 TGTAAAGTACCTCGCGCGGACACGC 558

RESULT 90
AL716984/c
LOCUS
DEFINITION
AL716984 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone EN0AA021ZA01 5', mRNA sequence.
ACCESSION
AL716984
VERSION
AL716984.1 GI:20181587
KEYWORDS
EST.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 572)
AUTHORS
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M.,
Hardelin,J.P., Weissenbach,J. and Petit,C.
TITLE
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
JOURNAL
Unpublished (2002)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1.572
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="EN0AA021ZA01"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match 1.5%; Score 26; DB 1; Length 572;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAAAGTACCTCGCGCGGACACGC 1713
Db 29 TGTAAAGTACCTCGCGCGGACACGC 4

RESULT 91
CF064307/c
LOCUS
CF064307 581 bp mRNA linear EST 21-JUL-2003
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```

DEFINITION   QCU9g04.yg QCU Zea mays cDNA clone QCU9g04, mRNA sequence.
ACCESSION    CF064307
VERSION      CF064307.1 GI:33104347
KEYWORDS     EST.
SOURCE       Zea mays
ORGANISM     Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 581)
AUTHORS      Genoplante.
TITLE        Genoplante, a major partnership french program in plant genomics
JOURNAL      Unpublished (2003)
COMMENT      Contact: Genoplante
              93, rue Henri Rochefort 91025 EVRY CEDEX France
              Tel: 33 1 69 47 54 00
              Fax: 33 1 69 47 54 10
              This sequence has been generated in the framework of the french
              plant genomics programme 'Genoplante' (http://www.genoplante.com
              and http://genoplante-info.infobiogen.fr).

FEATURES             Location/Qualifiers
     source           1..581
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cullivar="f333 or f334"
                     /db_xref="taxon:4577"
                     /clone="QCU9g04"
                     /issue_type="seedling minus kernel"
                     /clone_lib="QCU"

ORIGIN
Query Match      1.5%; Score 26; DB 6; Length 581;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    1688  TGTAACTACTCGCGCGGACACG 1713
      |||||
Db     28  TGTAACTACTCGCGCGGACACG 3

RESULT 92
BY753126
LOCUS      BY753126
DEFINITION BY753126 657 bp mRNA linear EST 17-DEC-2002
           CDNA clone F930111008 5', mRNA sequence.
ACCESSION  BY753126
VERSION    BY753126.1 GI:27184397
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
           Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 657)
AUTHORS    Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
           Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
           Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
           Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
           Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
           Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
           Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
           Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
           Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
           Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
           Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
           Kurochkin,I.V., Lee,V., Lenhard,B., Lyons,P.A., Maglott,D.R.,
           Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
           Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
           Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
           Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
           Sandelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K.,
           Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

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Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,I.G., Wyshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yaunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12456851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Wataniki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Kirk W. Beisel ( Boys Town National
Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
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ORIGIN
Query Match      1.5%; Score 26; DB 5; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    260  GGGCTGCCTTCGCTTCGCCCGCTGC 285
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RESULT 93
BI653517

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LOCUS BI653517 680 bp mRNA linear EST 12-SEP-2001
 DEFINITION 603300520F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5341085 5', mRNA sequence.

ACCESSION BI653517
 VERSION BI653517.1 GI:15567753
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 680)
 NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM1866 row: g column: 06
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FEATURES
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 /clone="IMAGE:5341085"
 /tissue_type="tumor, gross tissue"
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 /lab_host="DH10B"
 /clone_lib="NCI_CGAP Mam3"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."

ORIGIN
 Query Match 1.5%; Score 26; DB 3; Length 680;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 GGCTGCTTCTGCTTCGCGCGCTGC 285
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 Db 310 GGCTGCTTCTGCTTCGCGCGCTGC 335

RESULT 94
 BI156000
 LOCUS BI156000 685 bp mRNA linear EST 05-JUL-2001
 DEFINITION 602903535F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5033097 5', mRNA sequence.

ACCESSION BI156000
 VERSION BI156000.1 GI:14616001
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 685)
 NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM1092 row: f column: 10
 High quality sequence stop: 685.

FEATURES
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 /clone="IMAGE:5033097"
 /tissue_type="tumor, gross tissue"
 /dev_stage="10 months"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP Mam3"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."

ORIGIN
 Query Match 1.5%; Score 26; DB 2; Length 685;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 GGCTGCTTCTGCTTCGCGCGCTGC 285
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 Db 524 GGCTGCTTCTGCTTCGCGCGCTGC 549

RESULT 95
 DN478595/c
 LOCUS DN478595 692 bp mRNA linear EST 09-MAR-2005
 DEFINITION altr010xm17 A. brassicicola mycelial culture infecting B. oleracea
 Alternaria brassicicola cDNA clone altr010xm17, mRNA sequence.

ACCESSION DN478595
 VERSION DN478595.1 GI:60675906
 KEYWORDS EST.
 SOURCE Alternaria brassicicola
 ORGANISM Alternaria brassicicola

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.

1 (bases 1 to 692)
 Cramer,R.A., Craven,K.D., Thon,M.R., Cho,Y., Knudson,D.L., Mitchell,T.K. and Lawrence,C.B.
 Expressed Sequence Tag (EST) Analysis of a Compatible Alternaria brassicicola-Brassica oleracea Interaction
 Unpublished (2005)
 Contact: Dr. Thomas K. Mitchell
 Center for Integrated Fungal Research, NC State University
 851 Main Campus Dr. Suite 233, Raleigh, NC 27606, USA
 Tel: (919) 513-3926
 Fax: (919) 513-0024
 Email: thomas_mitchell@ncsu.edu
 Seq primer: T7 SP6 primer.

FEATURES
 source
 1..692
 /organism="Alternaria brassicicola"
 /mol_type="mRNA"
 /strain="ATCC 96866"
 /db_xref="taxon:29001"
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 /clone_lib="A. brassicicola mycelial culture infecting B. oleracea"
 /note="Vector: pGEMT; Mycelia Culture grown for 48 hours,

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24 degrees C, minimal media minus Nitrogen. Infecting
Brassica oleracea Var. Capitata cultivar 'tenderwestfl'"

ORIGIN

Query Match
Best Local Similarity 1.5%; Score 26; DB 8; Length 692;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGGCGCGACCAACGC 1713
Db 28 TGTAACTACTCGGCGCGACCAACGC 3

RESULT 96
CV943849
LOCUS
DEFINITION
CV943849 707 bp mRNA linear EST 25-JAN-2005
PU003E7 mycelium, subtracted infection mimic Phytophthora infestans
cDNA, mRNA sequence.
ACCESSION
CV943849.1 GI:58133605
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytophthora infestans (potato late blight agent)
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
1 (bases 1 to 707)
AUTHORS
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T., and Judelson, H.S.
Large-scale gene discovery in the oomycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
fungi
JOURNAL
PUBMED
15782637
COMMENT
Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
Contact: Judelson HS
Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers
FEATURES
source
1..707
/organism="Phytophthora infestans"
/mol_type="mRNA"
/strain="88069"
/db_xref="taxon:4787"
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/note="Vector: pSPORT1"

ORIGIN

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QY 1688 TGTAACTACTCGGCGCGACCAACGC 1713
Db 287 TGTAACTACTCGGCGCGACCAACGC 312

RESULT 97
BI409054
LOCUS
DEFINITION
BI409054 722 bp mRNA linear EST 14-AUG-2001
602961119F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5116780 5',
mRNA sequence.
ACCESSION
BI409054
VERSION
BI409054.1 GI:15169977
KEYWORDS
SOURCE
Mus musculus (house mouse)

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 722)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11284 row: e column: 05
High quality sequence stop: 720.
Location/Qualifiers
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/clone_lib="NCI CGAP Lu33"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAATGGAGCGCGCTCTGTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match
Best Local Similarity 1.5%; Score 26; DB 3; Length 722;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 GGGCTGCCCTTCGCTTCGCGCGCTGC 285
Db 440 GGGCTGCCCTTCGCTTCGCGCGCTGC 465

RESULT 98
CV944323
LOCUS
DEFINITION
CV944323 737 bp mRNA linear EST 25-JAN-2005
PU011H10 mycelium, subtracted infection mimic Phytophthora
infestans cDNA, mRNA sequence.
ACCESSION
CV944323
VERSION
CV944323.1 GI:58134079
KEYWORDS
SOURCE
Phytophthora infestans (potato late blight agent)
ORGANISM
Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
1 (bases 1 to 737)
AUTHORS
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T., and Judelson, H.S.
Large-scale gene discovery in the oomycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
fungi
TITLE

```

JOURNAL
FURNED
COMMENT

Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
15782637
Contact: Judelson HS
Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers
1. .737
/organism="Phytophthora infestans"
/mol_type="mRNA"
/strain="88069"
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/sex="Al"
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/note="Vector: pSPORT1"

FEATURES
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/note="Vector: pSPORT1"

ORIGIN
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1688 TGTAACTACCTCGCCCGCACCACGC 1713
|||||
Db 305 TGTAACTACCTCGCCCGCACCACGC 330
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RESULT 99
BI159562
LOCUS
DEFINITION
602919525F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5059854 5',
mRNA sequence.
BI159562 1 GI:14619563
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 746)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 742.

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/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam3"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI. Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

JOURNAL
FURNED
COMMENT

Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
15782637
Contact: Judelson HS
Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
Location/Qualifiers
1. .737
/organism="Phytophthora infestans"
/mol_type="mRNA"
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/db_xref="taxon:4787"
/sex="Al"
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/note="Vector: pSPORT1"

FEATURES
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/db_xref="taxon:4787"
/sex="Al"
/clone_lib="mycelium, substracted infection mimic"
/note="Vector: pSPORT1"

ORIGIN
Query Match 1.5%; Score 26; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1688 TGTAACTACCTCGCCCGCACCACGC 1713
|||||
Db 305 TGTAACTACCTCGCCCGCACCACGC 330
|||||

RESULT 99
BI159562
LOCUS
DEFINITION
602919525F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5059854 5',
mRNA sequence.
BI159562 1 GI:14619563
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 746)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 742.

FEATURES
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/clone="IMAGE:5059854"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam3"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI. Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

JOURNAL
FURNED
COMMENT

Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."

ORIGIN
Query Match 1.5%; Score 26; DB 2; Length 746;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 GGGCTGCTTCTGCTTCGCCGCTGC 285
|||||
Db 517 GGGCTGCTTCTGCTTCGCCGCTGC 542
|||||

RESULT 100
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LOCUS
DEFINITION
603166180F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5254507 5',
mRNA sequence.
BI905713 1 GI:16168280
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 746)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 746.

FEATURES
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Lu33"
/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCTCTGTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match 1.5%; Score 26; DB 3; Length 746;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 GGGCTGCTTCTGCTTCGCCGCTGC 285
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Db 420 GGGCTGCTTCTGCTTCGCCGCTGC 445
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Search completed: March 11, 2006, 23:47:04
Job time : 6327 secs

244	20	1.2	844	3	US-09-551-621A-76	Sequence 76, Appl	317	19	1.1	181	3	US-09-222-575-119	Sequence 119, App
245	20	1.2	844	3	US-10-076-622-77	Sequence 76, Appl	318	19	1.1	181	3	US-09-389-681-119	Sequence 119, App
246	20	1.2	72704	3	US-09-902-540-1273	Sequence 1273, Ap	319	19	1.1	181	3	US-09-620-405B-119	Sequence 119, App
C 247	19	1.1	20	3	US-09-284-782-11	Sequence 11, Appl	320	19	1.1	181	3	US-09-339-338-119	Sequence 119, App
C 248	19	1.1	20	3	US-09-323-873A-27	Sequence 27, Appl	321	19	1.1	181	3	US-09-433-826B-119	Sequence 119, App
C 249	19	1.1	20	3	US-09-455-486-29	Sequence 29, Appl	322	19	1.1	181	3	US-09-604-287A-119	Sequence 119, App
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C 251	19	1.1	20	3	US-10-027-807-10	Sequence 10, Appl	324	19	1.1	181	3	US-09-834-759-119	Sequence 119, App
C 252	19	1.1	20	3	US-10-027-807-13	Sequence 13, Appl	325	19	1.1	181	3	US-09-590-751A-119	Sequence 119, App
C 253	19	1.1	20	3	US-10-027-807-16	Sequence 16, Appl	326	19	1.1	181	3	US-09-551-621-119	Sequence 119, App
C 254	19	1.1	20	3	US-09-961-058-7	Sequence 7, Appl	327	19	1.1	181	3	US-09-551-621A-119	Sequence 119, App
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C 281	19	1.1	72	3	US-09-827-271-304	Sequence 304, App	C 354	19	1.1	204	3	US-09-401-064-66	Sequence 66, Appl
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c 403	19	1.1	226	3	US-09-827-271-79	Sequence 79, App1	476	19	1.1	300	3	US-09-685-166A-297	Sequence 297, App
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RESULT 1

US-10-104-047-799

; Sequence 799, Application US/10104047

; Patent No. 6943241

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. 6943241el full length cdNA

; FILE REFERENCE: H1-A0105

; CURRENT APPLICATION NUMBER: US/10/104,047

; PRIOR FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER:

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 799

; LENGTH: 1785

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-104-047-799

Query Match 93.1%; Score 1594; DB 3; Length 1785;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 90 ATGCCCGCCCTGGACACCCGCCCGCCAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG 149

QY 61 CGGCCAACAGACTATGTCTGGAGACATATGATTAACCACTTCAGCCCCCAACGCCGC 120

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241 TGGGTGTGGAGTGTGCTGGGCTGCTTCTGCTTCCGCGCTGCTGGGATTCCTCCAG 300
330 TGGGTGTGGAGTGTGCTGGGCTGCTTCTGCTTCCGCGCTGCTGGGATTCCTCCAG 389
301 CGCTGTGGAGCTGTGTGGGAGATGACGCCCTTGTCTGTACTAGAGATCCACTGAG 360
390 CGCTGTGGAGCTGTGTGGGAGATGACGCCCTTGTCTGTACTAGAGATCCACTGAG 449
361 GGGACTGCTGAAGCAACTGGGCAAGGAGACAAATGGAGTGCCTCCAGCCCTGATCGT 420
450 GGGACTGCTGAAGCAACTGGGCAAGGAGACAAATGGAGTGCCTCCAGCCCTGATCGT 509
421 GCACCCCGCCAGCGCGGGATGCGCAGCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAGC 480
510 GCACCCCGCCAGCGCGGGATGCGCAGCGGCTCAAGTCAACCATGGGCGAGCAGCTTCAGC 569
481 TACCCCGATGTTAAGCTCAAGAGCATCCCTGTATCCCTTACCCGAGGCGCACTCCCCA 540
570 TACCCCGATGTTAAGCTCAAGAGCATCCCTGTATCCCTTACCCGAGGCGCACTCCCCA 629
541 GCGCTGTAGCGGACCTCTGCTGCAAGGAGCCTGCGCGGATCCCGGATCCCGCATGGCAGAC 600
630 GCGCTGTAGCGGACCTCTGCTGCAAGGAGCCTGCGCGGATCCCGGATCCCGCATGGCAGAC 689
601 AGCTGTCCCGAGCCTTGTCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTCTTTCCAT 660
690 AGCTGTCCCGAGCCTTGTCCAGTAGTCTCTGCTGGCTCCGAGGAGTACTATTCTTTCCAT 749
661 GAGTGGGACCTGGACCTGCGGAGATGGGAGTGGCTCCATGTCGAGCCGAGAAATGTAT 720
750 GAGTGGGACCTGGACCTGCGGAGATGGGAGTGGCTCCATGTCGAGCCGAGAAATGTAT 809
721 GTGCTCATCTTCAAGAGCTGACAGAGCTGTTTCCAGGCTACACAGATCGATGAGCTGGCC 780
810 GTGCTCATCTTCAAGAGCTGACAGAGCTGTTTCCAGGCTACACAGATCGATGAGCTGGCC 869
781 AAGTGCACATCAGACACTGTGTTCTTGGAGAACACCAAGTAAAGATCTCGACCTTATCAGC 840
870 AAGTGCACATCAGACACTGTGTTCTTGGAGAACACCAAGTAAAGATCTCGACCTTATCAGC 929
841 AGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGCGCGCTTGGTACGCGGC 900
930 AGCATCAGCAGGACTACCACTGGATGAGCAGGATGCTGAGGCGCGCTTGGTACGCGGC 989
901 ATCATTTGCAATAGTACCGGAAAGAGCGGTGCTGCGCCACAGACCTCGGAGGTCGTTCA 960
990 ATCATTTGCAATAGTACCGGAAAGAGCGGTGCTGCGCCACAGACCTCGGAGGTCGTTCA 1049
961 ACTCGGGCTGTGCCCCCAACCGCTGTGCCCCCTGACAGTGGCCATCAGACCATGTTGGGC 1020
1050 ACTCGGGCTGTGCCCCCAACCGCTGTGCCCCCTGACAGTGGCCATGAGACCATGTTGGGC 1109
1021 TCAGGTCTCAGCCAGGATGAGTGCAGAGTCCAGGATCTCCAGGAGACGACTGCAGATGCC 1080
1110 TCAGGTCTCAGCCAGGATGAGTGCAGAGTCCAGGATCTCCAGGAGACGACTGCAGATGCC 1169
1081 ATGCCCCGGAAGCTGAGGCTTATGAGCTTCAAGGTATCCAGGATCCAGCAAGCATGACTCATCC 1140
1170 ATGCCCCGGAAGCTGAGGCTTATGAGCTTCAAGGTATCCAGGATCCAGCAAGCATGACTCATCC 1229
1141 TTCCAGGCGACCGACACAGACTGCTCGGGGCGACCCCTTGTCTCAGGTGACTGCTTAACCC 1200
1230 TTCCAGGCGACCGACACAGACTGCTCGGGGCGACCCCTTGTCTCAGGTGACTGCTGACCC 1289

1201 CTGCCAGGCGCCAGCTGCCACACCCCTTTCTGGGAGAAAGCATGGCCTACAGAAATGAAGAGG 1260
1290 CTGCCAGGCGCCAGCTGCCACACCCCTTTCTGGGAGAAAGCATGGCCTACAGAAATGAAGAGG 1349
1261 GGACCAAGGAACCCCTCTGGGAGAGGCTTAGACCTGAAGCAGTGCACCTCTGGCTCTCTCC 1320
1350 GGACCAAGGAACCCCTCTGGGAGAGGCTTAGACCTGAAGCAGTGCACCTCTGGCTCTCTCC 1409
1321 TGCCTTGGCTGACTGGGTTCTCTGGACCATGTGCAATTTCACTGGGCGCATGGGATCTACATC 1380
1410 TGCCTTGGCTGACTGGGTTCTCTGGACCATGTGCAATTTCACTGGGCGCATGGGATCTACATC 1469
1381 TCCTTCATCCCGCAGCTGGTCTGATCCCTGCGCAGAGGCCCTTCTCTCTCTCATGCTCT 1440
1470 TCCTTCATCCCGCAGCTGGTCTGATCCCTGCGCAGAGGCCCTTCTCTCTCTCATGCTCT 1529
1441 TCAGGTGGCTGATCATGGAAGTAAGGAGTTAGGCAATTAACCTTCTGGGAGTGAACCCCTG 1500
1530 TCAGGTGGCTGATCATGGAAGTAAGGAGTTAGGCAATTAACCTTCTGGGAGTGAACCCCTG 1589
1501 ACTCCATCCCGCTATTGGCCACCCTAACCAATCATGCAAACTTCTCCCTCTCCCTGGGTAAT 1560
1590 ACTCCATCCCGCTATTGGCCACCCTAACCAATCATGCAAACTTCTCCCTCTCCCTGGGTAAT 1649
1561 TCACAGTTAAAGAAAGCTTATCTTAAATGTATTTGTTGGGGGTGGGCGAGGCCCACT 1620
1650 TCACAGTTAAAGAAAGCTTATCTTAAATGTATTTGTTGGGGGTGGGCGAGGCCCACT 1709
1621 CTATGTTATGTTAAGGAGTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCT 1680
1710 CTATGTTATGTTAAGGAGTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCT 1769
1681 CACAGTTTCTAAGTAC 1696
1770 CACAGTTTCTAAGTAC 1785

RESULT 2

US-10-131-827-8473
; Sequence 8473, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8473
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(224)
; OTHER INFORMATION: n = A, C, T or G
US-10-131-827-8473

Query Match 1.5%; Score 25; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACTCTGGCGCGGACCAACGC 1713

```
Db      189 GTAAGTACTCGCGCGGACCAACGC 213
|||||
Query Match      1.3%; Score 23; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-10-131-827-8150
; Sequence 8150, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8150
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(170)
; OTHER INFORMATION: N = A, T, C or G
US-10-131-827-8150

Query Match      1.3%; Score 23; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1691 AAGTACTCGCGCGGACCAACGC 1713
Db      137 AAGTACTCGCGCGGACCAACGC 159
|||||

RESULT 4
US-09-328-475C-111/C
; Sequence 111, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(468)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-111
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Query Match      1.3%; Score 23; DB 3; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1691 AAGTACTCGCGCGGACCAACGC 1713
Db      104 AAGTACTCGCGCGGACCAACGC 82
|||||

RESULT 5
US-09-328-475C-246/C
; Sequence 246, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 246
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-246

Query Match      1.3%; Score 23; DB 3; Length 482;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1691 AAGTACTCGCGCGGACCAACGC 1713
Db      104 AAGTACTCGCGCGGACCAACGC 82
|||||

RESULT 6
US-09-328-475C-239/C
; Sequence 239, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 239
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(483)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-239
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Query Match      1.3%; Score 23; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 104 AAGTACCTCGCGCGGACCAACGC 82

RESULT 7
US-09-328-475C-224/c
; Sequence 224, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 224
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(494)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-224

Query Match      1.3%; Score 23; DB 3; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 103 AAGTACCTCGCGCGGACCAACGC 81

RESULT 8
US-09-328-475C-185/c
; Sequence 185, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo Sapien

Query Match      1.3%; Score 23; DB 3; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 100 AAGTACCTCGCGCGGACCAACGC 78

RESULT 9
US-09-328-475C-181/c
; Sequence 181, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 181
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(501)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-181

Query Match      1.3%; Score 23; DB 3; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 101 AAGTACCTCGCGCGGACCAACGC 79

RESULT 10
US-09-328-475C-196/c
; Sequence 196, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 196
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo Sapien
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 196
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(511)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-196

Query Match
Best Local Similarity 1.3%; Score 23; DB 3; Length 511;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 106 AAGTACCTCGCGCGGACCAACGC 84

RESULT 11
US-09-328-475C-305/c
; Sequence 305, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 305
; LENGTH: 719
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(719)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-305

Query Match
Best Local Similarity 1.3%; Score 23; DB 3; Length 719;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 99 AAGTACCTCGCGCGGACCAACGC 77

RESULT 12
US-09-328-475C-315/c
; Sequence 315, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
```

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; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 315
; LENGTH: 722
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(722)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-315

Query Match
Best Local Similarity 1.3%; Score 23; DB 3; Length 722;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 95 AAGTACCTCGCGCGGACCAACGC 73

RESULT 13
US-09-328-475C-277/c
; Sequence 277, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 277
; LENGTH: 724
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(724)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-277

Query Match
Best Local Similarity 1.3%; Score 23; DB 3; Length 724;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 100 AAGTACCTCGCGCGGACCAACGC 78

RESULT 14
US-09-328-475C-295
; Sequence 295, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
```

```
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 295
; LENGTH: 725
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(725)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-295

Query Match 1.3%; Score 23; DB 3; Length 725;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1691 AAGTACTCGGCGCGGACCACGC 1713
Db 598 AAGTACTCGGCGCGGACCACGC 620

RESULT 15
US-09-328-475C-329/c
; Sequence 329, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 329
; LENGTH: 725
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(725)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-329

Query Match 1.3%; Score 23; DB 3; Length 725;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1691 AAGTACTCGGCGCGGACCACGC 1713
Db 97 AAGTACTCGGCGCGGACCACGC 75

RESULT 16
US-09-328-475C-331/c
; Sequence 331, Application US/09328475C
; Patent No. 6476207
```

```
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 727
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(727)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-331

Query Match 1.3%; Score 23; DB 3; Length 727;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1691 AAGTACTCGGCGCGGACCACGC 1713
Db 98 AAGTACTCGGCGCGGACCACGC 76

RESULT 17
US-09-328-475C-294
; Sequence 294, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 294
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(736)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-294

Query Match 1.3%; Score 23; DB 3; Length 736;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1691 AAGTACTCGGCGCGGACCACGC 1713
Db 619 AAGTACTCGGCGCGGACCACGC 641
```



```
RESULT 18
US-09-328-475C-314/c
; Sequence 314, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 314
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(740)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-314

Query Match          1.3%; Score 23; DB 3; Length 740;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGGCGCGGACCACGC 1713
DB 123 AAGTACTCGGCGCGGACCACGC 101

RESULT 19
US-09-328-475C-304/c
; Sequence 304, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 304
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(741)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-304

Query Match          1.3%; Score 23; DB 3; Length 741;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1691 AAGTACTCGGCGCGGACCACGC 1713
DB 124 AAGTACTCGGCGCGGACCACGC 102

RESULT 20
US-09-328-475C-330/c
; Sequence 330, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 330
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(741)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-330

Query Match          1.3%; Score 23; DB 3; Length 741;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGGCGCGGACCACGC 1713
DB 122 AAGTACTCGGCGCGGACCACGC 100

RESULT 21
US-09-328-475C-276/c
; Sequence 276, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 276
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(744)
; OTHER INFORMATION: n = A,T,C or G
```

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US-09-328-475C-276
Query Match      1.3%; Score 23; DB 3; Length 744;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGGCGCGGACACG 1713
Db 123 AAGTACTCGGCGCGGACACG 101

RESULT 22
US-09-328-475C-328/c
; Sequence 328, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(747)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-328

Query Match      1.3%; Score 23; DB 3; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGGCGCGGACACG 1713
Db 122 AAGTACTCGGCGCGGACACG 100

RESULT 23
US-09-328-475C-158/c
; Sequence 158, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 772
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(772)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-158

Query Match      1.3%; Score 23; DB 3; Length 780;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACTCGGCGCGGACACG 1713
Db 107 AAGTACTCGGCGCGGACACG 85

RESULT 25
US-09-280-116-268
; Sequence 268, Application US/09280116A
; Patent No. 631427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 268
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: ubiquitin carboxyl-terminal hydrolases family 1
```

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(781)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-268

Query Match          1.3%; Score 23; DB 3; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGCGGACCAACGC 1713
Db 740 AAGTACCTCGGCGGCGGACCAACGC 762

RESULT 26
US-09-328-475C-167/c
; Sequence 167, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 167
; LENGTH: 797
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(797)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-167

Query Match          1.3%; Score 23; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGCGGACCAACGC 1713
Db 111 AAGTACCTCGGCGGCGGACCAACGC 89

RESULT 27
US-09-328-475C-229/c
; Sequence 229, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 229
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(815)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-229

Query Match          1.3%; Score 23; DB 3; Length 815;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGCGGACCAACGC 1713
Db 646 AAGTACCTCGGCGGCGGACCAACGC 668

RESULT 28
US-09-328-475C-240
; Sequence 240, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 240
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(815)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-240

Query Match          1.3%; Score 23; DB 3; Length 815;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGCGGACCAACGC 1713
Db 646 AAGTACCTCGGCGGCGGACCAACGC 668

RESULT 29
US-09-328-475C-249/c
; Sequence 249, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
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; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 249
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(821)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-249

Query Match      1.3%; Score 23; DB 3; Length 821;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1691 AAGTACTCGCGCGGACACGCG 1713
Db      80  AAGTACTCGCGCGGACACGCG 58

RESULT 30
US-09-328-475C-245/c
; Sequence 245, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 245
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(822)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-245

Query Match      1.3%; Score 23; DB 3; Length 822;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1691 AAGTACTCGCGCGGACACGCG 1713
Db      85  AAGTACTCGCGCGGACACGCG 63

RESULT 31
US-09-328-475C-191/c
; Sequence 191, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
```

```
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(823)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-191

Query Match      1.3%; Score 23; DB 3; Length 823;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1691 AAGTACTCGCGCGGACACGCG 1713
Db      82  AAGTACTCGCGCGGACACGCG 60

RESULT 32
US-09-328-475C-255/c
; Sequence 255, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 255
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(830)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-255

Query Match      1.3%; Score 23; DB 3; Length 830;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1691 AAGTACTCGCGCGGACACGCG 1713
Db      113 AAGTACTCGCGCGGACACGCG 91

RESULT 33
US-09-328-475C-43/c
; Sequence 43, Application US/09328475C
; Patent No. 6476207
```

```

; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1020)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-43

Query Match      1.3%; Score 23; DB 3; Length 1020;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGACCAACGC 1713
    |||||
Db 100 AAGTACCTCGGCGGACCAACGC 78

RESULT 34
US-09-328-475C-102
; Sequence 102, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1020)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-102

Query Match      1.3%; Score 23; DB 3; Length 1020;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGACCAACGC 1713
    |||||
Db 526 AAGTACCTCGGCGGACCAACGC 548
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RESULT 35
US-09-328-475C-103/c
; Sequence 103, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 103
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1021)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-103

Query Match      1.3%; Score 23; DB 3; Length 1021;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGGCGGACCAACGC 1713
    |||||
Db 101 AAGTACCTCGGCGGACCAACGC 79

RESULT 36
US-09-328-475C-51/c
; Sequence 51, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-51

Query Match      1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1691 AAGTACCTCGCGCGGACACGC 1713
Db 99 AAGTACCTCGCGCGGACACGC 77

RESULT 37
US-09-328-475C-56/c
; Sequence 56, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-56

Query Match 1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACACGC 1713
Db 111 AAGTACCTCGCGCGGACACGC 89

RESULT 38
US-09-328-475C-71/c
; Sequence 71, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-71
```

```
US-09-328-475C-71
Query Match 1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACACGC 1713
Db 100 AAGTACCTCGCGCGGACACGC 78

RESULT 39
US-09-328-475C-77/c
; Sequence 77, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-77

Query Match 1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACACGC 1713
Db 106 AAGTACCTCGCGCGGACACGC 84

RESULT 40
US-09-328-475C-78
; Sequence 78, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 1024
; TYPE: DNA
US-09-328-475C-78
```

```
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-78

Query Match          1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 515 AAGTACCTCGCGCGGACCAACGC 537

RESULT 41
US-09-328-475C-93/c
; Sequence 93, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532,002/200130,463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-93

Query Match          1.3%; Score 23; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 100 AAGTACCTCGCGCGGACCAACGC 78

RESULT 42
US-09-328-475C-334
; Sequence 334, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532,002/200130,463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2051)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-334

Query Match          1.3%; Score 23; DB 3; Length 2051;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 AAGTACCTCGCGCGGACCAACGC 1713
Db 1814 AAGTACCTCGCGCGGACCAACGC 1836

RESULT 43
US-09-902-540-8302
; Sequence 8302, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8302
; LENGTH: 2253
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8302

Query Match          1.3%; Score 23; DB 3; Length 2253;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 666 GGACCTGGACCTGCGCGAGATGG 688
Db 1188 GGACCTGGACCTGCGCGAGATGG 1210

RESULT 44
US-09-902-540-866
; Sequence 866, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 866
; LENGTH: 6339
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-866
```

Query Match 1.3%; Score 23; DB 3; Length 6339;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 666 GGACCTGGACCTGCGCGAGATGG 688
DB 1190 GGACCTGGACCTGCGCGAGATGG 1212

RESULT 45

US-09-188-930-4/c

; Sequence 4, Application US/09188930A

; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James Greg

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; FILE REFERENCE: 11000.1011c1

; CURRENT APPLICATION NUMBER: US/09/188,930A

; CURRENT FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 348

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 311

; TYPE: DNA

; ORGANISM: Human

US-09-188-930-4

Query Match 1.3%; Score 22; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCCAGC 1713
DB 23 AGTACTCGCGCGGACCCAGC 2

RESULT 46

US-09-312-283C-4/c

; Sequence 4, Application US/09312283C

; Patent No. 6573095

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James G.

; APPLICANT: Kumble, Krishanand D.

; TITLE OF INVENTION: Compositions Isolated from Skin Cells

; FILE REFERENCE: 11000.1011c2

; CURRENT APPLICATION NUMBER: US/09/312,283C

; CURRENT FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 425

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 311

; TYPE: DNA

; ORGANISM: Mouse

US-09-312-283C-4

Query Match 1.3%; Score 22; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCCAGC 1713
DB 23 AGTACTCGCGCGGACCCAGC 2

RESULT 47

US-10-002-344A-138

; Sequence 138, Application US/10002344A

; Patent No. 6846650

; GENERAL INFORMATION:

; APPLICANT: Recipon, Herve

; APPLICANT: Sun, Yongming

; APPLICANT: Chen, Sei-Yu

; APPLICANT: Liu, Chenghua

; APPLICANT: Turner, Leah

; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot

; FILE REFERENCE: DEX-0241

; CURRENT APPLICATION NUMBER: US/10/002,344A

; PRIOR FILING DATE: 2002-03-15

; PRIOR APPLICATION NUMBER: US 60/242,998

; NUMBER OF SEQ ID NOS: 277

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 138

; LENGTH: 352

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-002-344A-138

Query Match 1.3%; Score 22; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCCAGC 1713
DB 326 AGTACTCGCGCGGACCCAGC 347

RESULT 48

US-09-328-475C-237/c

; Sequence 237, Application US/09328475C

; Patent No. 6476207

; GENERAL INFORMATION:

; APPLICANT: Zhang, Jimmy

; APPLICANT: Astel, Jon H.

; APPLICANT: Carroil III, Eddie

; APPLICANT: Endege, Wilson O.

; APPLICANT: Ford, Donna M.

; APPLICANT: Monahan, John B.

; APPLICANT: Schlegel, Robert

; APPLICANT: Steinmann, Kathleen E.

; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT

; FILE REFERENCE: 1532.002/200130.463

; CURRENT APPLICATION NUMBER: US/09/328,475C

; CURRENT FILING DATE: 1999-06-09

; NUMBER OF SEQ ID NOS: 341

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 237

; LENGTH: 483

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(483)

; OTHER INFORMATION: n = A,T,C or G

US-09-328-475C-237

Query Match 1.3%; Score 22; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCCAGC 1713
DB 103 AGTACTCGCGCGGACCCAGC 82


```
RESULT 49
US-09-328-475C-222/c
; Sequence 222, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 222
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-222

Query Match          1.3%; Score 22; DB 3; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
DB 103 AGTACTCGCGCGGACACGC 82

RESULT 50
US-09-328-475C-194
; Sequence 194, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 194
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-194

Query Match          1.3%; Score 22; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
DB 309 AGTACTCGCGCGGACACGC 330

RESULT 51
US-09-328-475C-200/c
```

```
; Sequence 200, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 200
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(506)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-200

Query Match          1.3%; Score 22; DB 3; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
DB 104 AGTACTCGCGCGGACACGC 83

RESULT 52
US-10-131-827-8248
; Sequence 8248, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8248
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8248

Query Match          1.3%; Score 22; DB 3; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
DB 568 AGTACTCGCGCGGACACGC 589

RESULT 53
```

US-09-328-475C-281/c
; Sequence 281, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 727
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(727)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-281

Query Match 1.3%; Score 22; DB 3; Length 727;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCGC 1713
DB 97 AGTACTCGCGCGGACCGC 76

RESULT 54
US-09-328-475C-280/c
; Sequence 280, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 751
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(751)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-280

Query Match 1.3%; Score 22; DB 3; Length 751;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCGC 1713

DB 122 AGTACTCGCGCGGACCGC 101

RESULT 55
US-09-328-475C-169
; Sequence 169, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 169
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(771)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-169

Query Match 1.3%; Score 22; DB 3; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCGC 1713
DB 291 AGTACTCGCGCGGACCGC 312

RESULT 56
US-09-328-475C-176/c
; Sequence 176, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(773)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-176

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Query Match          1.3%; Score 22; DB 3; Length 773;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACACGC 1713
DB 86 AGTACTCTGGCGCGGACACGC 65

RESULT 57
US-09-328-475C-163/c
; Sequence 163, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 776
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(776)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-163

Query Match          1.3%; Score 22; DB 3; Length 776;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACACGC 1713
DB 101 AGTACTCTGGCGCGGACACGC 80

RESULT 58
US-09-328-475C-168/c
; Sequence 168, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 168
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(780)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-168

Query Match          1.3%; Score 22; DB 3; Length 780;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACACGC 1713
DB 102 AGTACTCTGGCGCGGACACGC 81

RESULT 59
US-09-328-475C-119/c
; Sequence 119, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 119
; LENGTH: 811
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(811)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-119

Query Match          1.3%; Score 22; DB 3; Length 811;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCTGGCGCGGACACGC 1713
DB 81 AGTACTCTGGCGCGGACACGC 60

RESULT 60
US-09-328-475C-238
; Sequence 238, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 238
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(815)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-238

Query Match      1.3%; Score 22; DB 3; Length 815;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1692 AGTACCTCGCGCGGACCAACGC 1713
Db      496 AGTACCTCGCGCGGACCAACGC 517

RESULT 61
US-09-328-475C-223
; Sequence 223, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 223
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(822)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-223

Query Match      1.3%; Score 22; DB 3; Length 822;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1692 AGTACCTCGCGCGGACCAACGC 1713
Db      506 AGTACCTCGCGCGGACCAACGC 527

RESULT 62
US-09-328-475C-195/c
; Sequence 195, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
```

```
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 195
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(848)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-195

Query Match      1.3%; Score 22; DB 3; Length 848;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1692 AGTACCTCGCGCGGACCAACGC 1713
Db      99 AGTACCTCGCGCGGACCAACGC 78

RESULT 63
US-09-328-475C-104/c
; Sequence 104, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1017)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-104

Query Match      1.3%; Score 22; DB 3; Length 1017;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1692 AGTACCTCGCGCGGACCAACGC 1713
Db      101 AGTACCTCGCGCGGACCAACGC 80

RESULT 64
US-09-328-475C-57/c
; Sequence 57, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
```

```
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-57

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCCACGC 1713
Db 103 AGTACTCGCGCGGACCCACGC 82

RESULT 65
US-09-328-475C-61
; Sequence 61, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-61

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCCACGC 1713
Db 665 AGTACTCGCGCGGACCCACGC 686

RESULT 66
US-09-328-475C-62/c
; Sequence 62, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
```

```
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-62

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCCACGC 1713
Db 104 AGTACTCGCGCGGACCCACGC 83

RESULT 67
US-09-328-475C-65/c
; Sequence 65, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-65

Query Match          1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACCCACGC 1713
Db 103 AGTACTCGCGCGGACCCACGC 82
```

```
RESULT 68
US-09-328-475C-73/c
; Sequence 73, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-73

Query Match 1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACCTCGCGCGGACCCAGC 1713
Db 105 AGTACCTCGCGCGGACCCAGC 84

RESULT 69
US-09-328-475C-75/c
; Sequence 75, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-75

Query Match 1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-328-475C-79
; Sequence 79, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-79

Query Match 1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACCTCGCGCGGACCCAGC 1713
Db 399 AGTACCTCGCGCGGACCCAGC 420

RESULT 70
US-09-328-475C-79
; Sequence 79, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-79

Query Match 1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACCTCGCGCGGACCCAGC 1713
Db 399 AGTACCTCGCGCGGACCCAGC 420

RESULT 71
US-09-328-475C-80/c
; Sequence 80, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-80

Query Match 1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Query Match      1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
Db 110 AGTACTCGCGCGGACACGC 89

RESULT 72
US-09-328-475C-82/c
; Sequence 82, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)---(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-82

Query Match      1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
Db 104 AGTACTCGCGCGGACACGC 83

RESULT 73
US-09-328-475C-86/c
; Sequence 86, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)---(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-86

Query Match      1.3%; Score 22; DB 3; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
Db 111 AGTACTCGCGCGGACACGC 90

RESULT 74
US-09-188-930-249/c
; Sequence 249, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 249
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Human
US-09-188-930-249

Query Match      1.3%; Score 22; DB 3; Length 1212;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGGACACGC 1713
Db 24 AGTACTCGCGCGGACACGC 3

RESULT 75
US-09-312-283C-249/c
; Sequence 249, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-249

Query Match      1.3%; Score 22; DB 3; Length 1212;
Best Local Similarity 100.0%; Pred. No. 1.9;
```

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 AGTACTCGCGCGACACGC 1713
|||||
Db 24 AGTACTCGCGCGACACGC 3

RESULT 76

US-10-131-827-8652
; Sequence 8652, Application US/10131827

; Patent No. 6905827

; GENERAL INFORMATION:

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

; FILE REFERENCE: 506612000120

; CURRENT APPLICATION NUMBER: US/10/131,827

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764

; PRIOR FILING DATE: 2001-06-08

; NUMBER OF SEQ ID NOS: 9090

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8652

; LENGTH: 159

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-131-827-8652

Query Match 1.2%; Score 21; DB 3; Length 159;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACTCGCGCGACACGC 1713
|||||

Db 128 GTACTCGCGCGACACGC 148

RESULT 77

US-10-131-827-8632
; Sequence 8632, Application US/10131827

; Patent No. 6905827

; GENERAL INFORMATION:

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

; FILE REFERENCE: 506612000120

; CURRENT APPLICATION NUMBER: US/10/131,827

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764

; PRIOR FILING DATE: 2001-06-08

; NUMBER OF SEQ ID NOS: 9090

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8632

; LENGTH: 240

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-131-827-8632

Query Match 1.2%; Score 21; DB 3; Length 240;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACTCGCGCGACACGC 1713
|||||

Db 128 GTACTCGCGCGACACGC 148

RESULT 78

US-09-389-681-319
; Sequence 319, Application US/09389681A

; Patent No. 6518237

; GENERAL INFORMATION:

; APPLICANT: Yuqui, Jiang

; APPLICANT: Dillon, Devin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

; FILE REFERENCE: 210121.47003

; CURRENT APPLICATION NUMBER: US/09/389,681A

; CURRENT FILING DATE: 1999-09-02

; NUMBER OF SEQ ID NOS: 463

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 319

; LENGTH: 241

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(241)

; OTHER INFORMATION: n = A,T,C or G

US-09-389-681-319

Query Match 1.2%; Score 21; DB 3; Length 241;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACTCGCGCGACACGC 1713
|||||

Db 208 GTACTCGCGCGACACGC 228

RESULT 79

US-09-620-405B-319
; Sequence 319, Application US/09620405B

; Patent No. 6528054

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Dillon, Devin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Hepler, William T.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.47008

; CURRENT APPLICATION NUMBER: US/09/620,405B

; CURRENT FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 495

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 319

; LENGTH: 241

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(241)

; OTHER INFORMATION: n = A,T,C or G

US-09-620-405B-319

Query Match 1.2%; Score 21; DB 3; Length 241;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACTCGCGCGACACGC 1713
|||||

Db 208 GTACTCGCGCGACACGC 228


```
Db      208 GTACCTCGGCGCGACCAAGC 228

RESULT 80
US-09-433-826B-319
; Sequence 319, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-433-826B-319

Query Match      1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1693 GTACCTCGGCGCGACCAAGC 1713
|||||
Db      208 GTACCTCGGCGCGACCAAGC 228

RESULT 81
US-09-604-287A-319
; Sequence 319, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-604-287A-319

Query Match      1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1693 GTACCTCGGCGCGACCAAGC 1713
|||||
Db      208 GTACCTCGGCGCGACCAAGC 228

RESULT 82
US-09-834-759-319
; Sequence 319, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-759-319

Query Match      1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1693 GTACCTCGGCGCGACCAAGC 1713
|||||
Db      208 GTACCTCGGCGCGACCAAGC 228

RESULT 83
US-09-590-751A-319
; Sequence 319, Application US/09590751A
; Patent No. 6756477
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C6
; CURRENT APPLICATION NUMBER: US/09/590,751A
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-590-751A-319

Query Match      1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1693 GTACCTCGGCGCGACCAAGC 1713
|||||
Db      208 GTACCTCGGCGCGACCAAGC 228

RESULT 84
US-09-590-751A-319
; Sequence 319, Application US/09590751A
; Patent No. 6756477
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C6
; CURRENT APPLICATION NUMBER: US/09/590,751A
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-590-751A-319

Query Match      1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1693 GTACCTCGGCGCGACCAAGC 1713
|||||
Db      208 GTACCTCGGCGCGACCAAGC 228
```

Db 208 GTACCTCGGCGCGACACGC 228
|||||
RESULT 84
US-09-551-621-319
; Sequence 319, Application US/09551621
; Patent No. 6825175
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C5
; CURRENT APPLICATION NUMBER: US/09/551,621
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-551-621-319
Query Match 1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGGCGCGACACGC 1713
|||||
Db 208 GTACCTCGGCGCGACACGC 228
RESULT 85
US-09-551-621A-319
; Sequence 319, Application US/09551621A
; Patent No. 6844325
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C5
; CURRENT APPLICATION NUMBER: US/09/551,621A
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-551-621A-319
Query Match 1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGGCGCGACACGC 1713
|||||

Db 208 GTACCTCGGCGCGACACGC 228
RESULT 86
US-10-076-622-319
; Sequence 319, Application US/10076622
; Patent No. 6958361
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 24, 36, 39
; OTHER INFORMATION: n = A,T,C or G
US-10-076-622-319
Query Match 1.2%; Score 21; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGGCGCGACACGC 1713
|||||
Db 208 GTACCTCGGCGCGACACGC 228
RESULT 87
US-09-439-313-293
; Sequence 293, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-293
Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 GTACCTCGGCGCGACACGC 1713
|||||
Db 232 GTACCTCGGCGCGACACGC 252
|||||

Query Match	Best Local Similarity	Score 21;	DB 3;	Length 301;
Matches 21;	Conservative	0;	Mismatches	0; Indels
0;	Gaps	0;		
<p>FILE REFERENCE: 210121.428C5</p> <p>CURRENT APPLICATION NUMBER: US/09/159,812A</p> <p>CURRENT FILING DATE: 1998-09-23</p> <p>NUMBER OF SEQ ID NOS: 306</p> <p>SOFTWARE: FastSeq for Windows Version 3.0</p> <p>SEQ ID NO 293</p> <p>LENGTH: 301</p> <p>TYPE: DNA</p> <p>ORGANISM: Homo sapien</p> <p>US-09-159-812-293</p>				
Query Match	Best Local Similarity	Score 21;	DB 3;	Length 301;
Matches 21;	Conservative	0;	Mismatches	0; Indels
0;	Gaps	0;		
<p>1693 GTACCTCGGCGCGACACGCG 1713</p> <p>232 GTACCTCGGCGCGACACGCG 252</p>				
<p>RESULT 91</p> <p>US-09-636-215-293</p> <p>Sequence 293, Application US/09636215</p> <p>Patent No. 6620922</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Xu, Jiangchun</p> <p>APPLICANT: Dillon, Davin C.</p> <p>APPLICANT: Mitcham, Jennifer L.</p> <p>APPLICANT: Harlocker, Susan L.</p> <p>APPLICANT: Jiang, Yuqui</p> <p>APPLICANT: Henderson, Robert A.</p> <p>APPLICANT: Kalos, Michael D.</p> <p>APPLICANT: Fanger, Gary R.</p> <p>APPLICANT: Retter, Marc W.</p> <p>APPLICANT: Stolk, John A.</p> <p>APPLICANT: Day, Craig H.</p> <p>APPLICANT: Vedwick, Thomas S.</p> <p>APPLICANT: Carter, Darrick</p> <p>APPLICANT: Li, Samuel</p> <p>APPLICANT: Wang, Aijun</p> <p>APPLICANT: Skeiky, Yasir A.W.</p> <p>APPLICANT: Hepler, William</p> <p>TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND</p> <p>TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER</p> <p>FILE REFERENCE: 210121.42717C17</p> <p>CURRENT APPLICATION NUMBER: US/09/636,215</p> <p>CURRENT FILING DATE: 2000-08-10</p> <p>NUMBER OF SEQ ID NOS: 852</p> <p>SOFTWARE: FastSeq for Windows Version 3.0</p> <p>SEQ ID NO 293</p> <p>LENGTH: 301</p> <p>TYPE: DNA</p> <p>ORGANISM: Homo sapien</p> <p>US-09-636-215-293</p>				
Query Match	Best Local Similarity	Score 21;	DB 3;	Length 301;
Matches 21;	Conservative	0;	Mismatches	0; Indels
0;	Gaps	0;		
<p>1693 GTACCTCGGCGCGACACGCG 1713</p> <p>232 GTACCTCGGCGCGACACGCG 252</p>				
<p>RESULT 92</p> <p>US-09-685-166A-293</p> <p>Sequence 293, Application US/09685166A</p> <p>Patent No. 6630305</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Xu, Jiangchun</p> <p>APPLICANT: Dillon, Davin C.</p> <p>APPLICANT: Mitcham, Jennifer L.</p> <p>APPLICANT: Harlocker, Susan L.</p>				

; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGCGCGGACACGC 1713
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Db 232 GTACCTCGCGCGGACACGC 252

RESULT 93
US-09-688-489-293
; Sequence 293, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGCGCGGACACGC 1713
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Db 232 GTACCTCGCGCGGACACGC 252

RESULT 94
US-09-679-426-293
; Sequence 293, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGCGCGGACACGC 1713
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Db 232 GTACCTCGCGCGGACACGC 252

RESULT 95
US-09-759-143-293
; Sequence 293, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGCGACACGC 1713
Db 232 GTACCTCGGCGCGACACGC 252

RESULT 96

US-09-651-236-293
; Sequence 293, Application US/09651236
; Patent No. 6818751

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236

; CURRENT FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 865

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 293

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-651-236-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGCGACACGC 1713
Db 232 GTACCTCGGCGCGACACGC 252

RESULT 97

US-09-657-279-293
; Sequence 293, Application US/09657279
; Patent No. 6894146

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C19

; CURRENT APPLICATION NUMBER: US/09/657,279

; CURRENT FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 877

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 293

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-657-279-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGCGACACGC 1713
Db 232 GTACCTCGGCGCGACACGC 252

RESULT 98

US-10-012-896-293
; Sequence 293, Application US/10012896
; Patent No. 6943236

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Day, Craig H.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C27

; CURRENT APPLICATION NUMBER: US/10/012,896

; CURRENT FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 1011

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 293

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-012-896-293

Query Match 1.2%; Score 21; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGCGACACGC 1713
Db 232 GTACCTCGGCGCGACACGC 252

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US-10-131-827-8546
; Sequence 8546, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8546
; LENGTH: 311
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8546

Query Match      1.2%; Score 21; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGGCGGACACGC 1713
DB 280 GTACCTCGGCGGACACGC 300

RESULT 100
US-09-188-930-71/c
; Sequence 71, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Human
US-09-188-930-71

Query Match      1.2%; Score 21; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 23 GTACCTCGGCGGACACGC 3

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-989-890-105

Perfect score: 1713

Sequence: 1 atgccccgcctggacaccc.....tacctggcgcggaccacgc 1713

Scoring table: OMCO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 8

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1594	93.1	1785	6	US-10-104-047-799
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6	378	22.1	386	3	US-09-989-890-104
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8	334	19.5	393	9	US-10-779-543-10096
9	321	18.7	427	9	US-10-779-543-12051
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12	249	14.5	300	9	US-10-779-543-34
13	222	13.0	654	5	US-10-074-475-124
14	120	7.0	120	3	US-09-989-920-116
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22	25	1.5	310	3	US-09-814-353-11387
23	25	1.5	453	5	US-10-060-036-4393

463	1.5	25	24	3	US-09-814-353-17771	Sequence 17771, A
810	1.5	25	c	5	US-10-074-511-10	Sequence 10, Appl
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232	1.4	24	c	9	US-10-477-445-15	Sequence 15, Appl
253	1.4	24	c	9	US-09-814-353-17222	Sequence 17222, A
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274	1.4	24	c	3	US-09-814-353-11632	Sequence 11632, A
283	1.4	24	c	3	US-09-814-353-16395	Sequence 16395, A
310	1.4	24	c	3	US-09-814-353-3678	Sequence 3678, Ap
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312	1.4	24	c	3	US-09-814-353-10381	Sequence 10381, A
319	1.4	24	c	3	US-09-814-353-2936	Sequence 2936, Ap
319	1.4	24	c	3	US-09-814-353-9305	Sequence 9305, Ap
320	1.4	24	c	3	US-09-969-034-1870	Sequence 1870, A
326	1.4	24	c	8	US-09-814-353-17947	Sequence 17947, A
346	1.4	24	c	8	US-10-357-930-7995	Sequence 7995, Ap
368	1.4	24	c	3	US-09-814-353-4711	Sequence 4711, Ap
368	1.4	24	c	3	US-09-814-353-11010	Sequence 11010, A
370	1.4	24	c	3	US-09-814-353-5958	Sequence 5958, Ap
370	1.4	24	c	3	US-09-814-353-12238	Sequence 12238, A
376	1.4	24	c	8	US-10-357-930-6066	Sequence 6066, Ap
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391	1.4	24	c	3	US-09-814-353-2902	Sequence 2902, Ap
391	1.4	24	c	3	US-09-814-353-9231	Sequence 9231, Ap
392	1.4	24	c	3	US-09-814-353-16375	Sequence 16375, A
392	1.4	24	c	3	US-09-814-353-3267	Sequence 3267, Ap
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421	1.4	24	c	3	US-09-814-353-15689	Sequence 15689, A
421	1.4	24	c	3	US-09-814-353-5813	Sequence 5813, Ap
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425	1.4	24	c	5	US-10-198-846-7580	Sequence 7580, Ap
426	1.4	24	c	8	US-10-357-930-6566	Sequence 6566, Ap
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442	1.4	24	c	3	US-09-814-353-9426	Sequence 9426, Ap
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446	1.4	24	c	3	US-09-814-353-4306	Sequence 4306, Ap
446	1.4	24	c	3	US-09-814-353-10610	Sequence 10610, A
446	1.4	24	c	8	US-10-357-930-36059	Sequence 36059, A
446	1.4	24	c	8	US-10-357-930-37991	Sequence 37991, A
457	1.4	24	c	5	US-10-001-857-66	Sequence 66, Appl
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463	1.4	24	c	5	US-10-198-846-5501	Sequence 5501, Ap
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464	1.4	24	c	3	US-09-814-353-9665	Sequence 9665, Ap
471	1.4	24	c	3	US-09-814-353-15851	Sequence 15851, A
486	1.4	24	c	3	US-09-814-353-4472	Sequence 4472, Ap
486	1.4	24	c	3	US-09-814-353-10775	Sequence 10775, A
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517	1.4	24	c	3	US-09-814-353-15976	Sequence 15976, A
521	1.4	24	c	3	US-09-814-353-4993	Sequence 4993, Ap
521	1.4	24	c	3	US-09-814-353-11286	Sequence 11286, A
521	1.4	24	c	3	US-09-814-353-15615	Sequence 15615, A
524	1.4	24	c	3	US-09-814-353-17892	Sequence 17892, A
534	1.4	24	c	3	US-09-814-353-5823	Sequence 5823, Ap
534	1.4	24	c	3	US-09-814-353-12105	Sequence 12105, A
546	1.4	24	c	3	US-09-814-353-17394	Sequence 17394, A
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	C 100	24	1.4	610	9	US-10-950-009-112	Sequence 112, App	C 173	23	1.3	172	3	US-09-814-353-6223	Sequence 6223, Ap
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	C 106	24	1.4	646	3	US-09-814-353-11825	Sequence 11825, A	C 179	23	1.3	176	8	US-09-814-353-18831	Sequence 18831, A
	C 107	24	1.4	658	5	US-10-198-846-9185	Sequence 9185, Ap	C 180	23	1.3	176	8	US-10-357-930-7594	Sequence 7594, A
	C 108	24	1.4	687	3	US-09-814-353-18264	Sequence 18264, A	C 181	23	1.3	177	3	US-09-814-353-4470	Sequence 4470, Ap
	C 109	24	1.4	739	3	US-09-814-353-3699	Sequence 3699, Ap	C 182	23	1.3	177	3	US-09-814-353-4570	Sequence 4570, Ap
	C 110	24	1.4	739	3	US-09-814-353-10011	Sequence 10011, A	C 183	23	1.3	177	3	US-09-814-353-10773	Sequence 10773, A
	C 111	24	1.4	757	8	US-10-357-930-9069	Sequence 9069, Ap	C 184	23	1.3	177	3	US-09-814-353-10871	Sequence 10871, A
	C 112	24	1.4	787	9	US-10-858-412-28	Sequence 28, Appl	C 185	23	1.3	177	3	US-09-814-353-18680	Sequence 18680, A
	C 113	24	1.4	818	7	US-10-416-907-37	Sequence 37, Appl	C 186	23	1.3	177	9	US-10-357-930-35949	Sequence 35949, A
	C 114	24	1.4	872	5	US-10-198-846-4348	Sequence 4348, Ap	C 187	23	1.3	177	9	US-10-950-009-993	Sequence 993, App
	C 115	24	1.4	894	5	US-10-198-846-5595	Sequence 5595, Ap	C 188	23	1.3	178	3	US-09-814-353-6340	Sequence 6340, Ap
	C 116	23	1.3	25	10	US-11-036-317-802175	Sequence 802175, A	C 189	23	1.3	178	3	US-09-814-353-12618	Sequence 12618, A
	C 117	23	1.3	42	6	US-10-125-968-1413	Sequence 1413, Ap	C 190	23	1.3	178	8	US-10-357-930-8192	Sequence 8192, Ap
	C 118	23	1.3	43	3	US-09-732-560-3	Sequence 3, Appl1	C 191	23	1.3	179	3	US-09-814-353-4765	Sequence 4765, Ap
	C 119	23	1.3	43	6	US-10-125-968-1053	Sequence 1053, Ap	C 192	23	1.3	179	3	US-09-814-353-11062	Sequence 11062, A
	C 120	23	1.3	45	3	US-09-732-560-16	Sequence 16, Appl	C 193	23	1.3	179	9	US-10-950-009-859	Sequence 859, App
	C 121	23	1.3	46	6	US-10-125-968-1415	Sequence 1415, Ap	C 194	23	1.3	180	8	US-10-357-930-7349	Sequence 7349, Ap
	C 122	23	1.3	54	3	US-09-732-560-60	Sequence 60, Appl	C 195	23	1.3	181	3	US-09-814-353-18074	Sequence 18074, A
	C 123	23	1.3	60	3	US-09-732-560-61	Sequence 61, Appl	C 196	23	1.3	181	8	US-10-357-930-38113	Sequence 38113, A
	C 124	23	1.3	79	3	US-09-732-560-80	Sequence 80, Appl	C 197	23	1.3	183	3	US-09-814-353-4398	Sequence 4398, Ap
	C 125	23	1.3	85	3	US-09-732-560-116	Sequence 116, App	C 198	23	1.3	183	3	US-09-814-353-10897	Sequence 10897, A
	C 126	23	1.3	88	3	US-09-814-353-18926	Sequence 18926, A	C 199	23	1.3	184	8	US-10-357-930-37334	Sequence 37334, A
	C 127	23	1.3	92	3	US-09-732-560-110	Sequence 110, App	C 200	23	1.3	186	8	US-10-357-930-38155	Sequence 38155, A
	C 128	23	1.3	92	3	US-09-814-353-18278	Sequence 18278, A	C 201	23	1.3	187	8	US-10-357-930-7985	Sequence 7985, Ap
	C 129	23	1.3	94	9	US-10-950-009-938	Sequence 938, App	C 202	23	1.3	187	8	US-10-357-930-37729	Sequence 37729, A
	C 130	23	1.3	96	3	US-09-814-353-18596	Sequence 18596, A	C 203	23	1.3	188	3	US-09-814-353-5626	Sequence 5626, Ap
	C 131	23	1.3	103	8	US-10-357-930-7855	Sequence 7855, Ap	C 204	23	1.3	188	3	US-09-814-353-11913	Sequence 11913, A
	C 132	23	1.3	104	6	US-10-125-968-1402	Sequence 1402, Ap	C 205	23	1.3	188	8	US-10-357-930-7585	Sequence 7585, Ap
	C 133	23	1.3	111	3	US-09-732-560-42	Sequence 42, Appl	C 206	23	1.3	189	3	US-09-814-353-16163	Sequence 16163, A
	C 134	23	1.3	114	8	US-10-357-930-37310	Sequence 37310, A	C 207	23	1.3	190	3	US-09-814-353-3622	Sequence 3622, Ap
	C 135	23	1.3	117	9	US-10-950-009-845	Sequence 845, App	C 208	23	1.3	190	3	US-09-814-353-9936	Sequence 9936, Ap
	C 136	23	1.3	119	3	US-09-732-560-45	Sequence 45, Appl	C 209	23	1.3	190	8	US-10-357-930-37701	Sequence 37701, A
	C 137	23	1.3	122	6	US-10-125-968-1322	Sequence 1322, Ap	C 210	23	1.3	191	3	US-09-814-353-18492	Sequence 18492, A
	C 138	23	1.3	127	3	US-09-814-353-6064	Sequence 6064, Ap	C 211	23	1.3	191	8	US-10-357-930-7331	Sequence 7331, Ap
	C 139	23	1.3	127	3	US-09-814-353-12343	Sequence 12343, A	C 212	23	1.3	193	8	US-10-357-930-37634	Sequence 37634, A
	C 140	23	1.3	128	3	US-09-814-353-5052	Sequence 5052, Ap	C 213	23	1.3	195	3	US-09-814-353-5805	Sequence 5805, Ap
	C 141	23	1.3	128	3	US-09-814-353-11344	Sequence 11344, A	C 214	23	1.3	195	3	US-09-814-353-12088	Sequence 12088, A
	C 142	23	1.3	133	3	US-09-814-353-5393	Sequence 5393, Ap	C 215	23	1.3	195	3	US-09-814-353-18727	Sequence 18727, A
	C 143	23	1.3	133	3	US-09-814-353-11680	Sequence 11680, A	C 216	23	1.3	195	8	US-10-357-930-37485	Sequence 37485, A
	C 144	23	1.3	136	8	US-10-357-930-7452	Sequence 7452, Ap	C 217	23	1.3	196	8	US-10-357-930-36921	Sequence 36921, A
	C 145	23	1.3	140	3	US-09-814-353-17414	Sequence 17414, A	C 218	23	1.3	196	8	US-10-357-930-38099	Sequence 38099, A
	C 146	23	1.3	142	3	US-09-814-353-4669	Sequence 4669, Ap	C 219	23	1.3	198	3	US-09-732-560-26	Sequence 26, Appl
	C 147	23	1.3	142	3	US-09-814-353-10968	Sequence 10968, A	C 220	23	1.3	198	3	US-09-814-353-4802	Sequence 4802, Ap
	C 148	23	1.3	142	8	US-10-357-930-37807	Sequence 37807, A	C 221	23	1.3	198	3	US-09-814-353-11099	Sequence 11099, A
	C 149	23	1.3	143	3	US-09-814-353-18749	Sequence 18749, A	C 222	23	1.3	200	3	US-09-814-353-6265	Sequence 6265, Ap
	C 150	23	1.3	147	3	US-09-814-353-5092	Sequence 5092, Ap	C 223	23	1.3	200	3	US-09-814-353-12543	Sequence 12543, A
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	C 152	23	1.3	147	3	US-09-814-353-11384	Sequence 11384, A	C 225	23	1.3	203	3	US-09-814-353-5532	Sequence 5532, Ap
	C 153	23	1.3	149	3	US-09-814-353-5529	Sequence 5529, Ap	C 226	23	1.3	203	3	US-09-814-353-11819	Sequence 11819, A
	C 154	23	1.3	149	8	US-10-357-930-7423	Sequence 7423, Ap	C 227	23	1.3	203	3	US-09-814-353-18739	Sequence 18739, A
	C 155	23	1.3	150	3	US-09-814-353-17146	Sequence 17146, A	C 228	23	1.3	203	3	US-09-814-353-18771	Sequence 18771, A
	C 156	23	1.3	150	8	US-10-357-930-37363	Sequence 37363, A	C 229	23	1.3	205	3	US-09-814-353-18249	Sequence 18249, A
	C 157	23	1.3	151	3	US-09-814-353-6037	Sequence 6037, Ap	C 230	23	1.3	206	3	US-09-814-353-18427	Sequence 18427, A
	C 158	23	1.3	151	3	US-09-814-353-12316	Sequence 12316, Ap	C 231	23	1.3	207	3	US-09-732-560-48	Sequence 48, Appl
	C 159	23	1.3	151	3	US-09-814-353-12316	Sequence 12316, A	C 232	23	1.3	207	8	US-10-357-930-7941	Sequence 7941, Ap
	C 160	23	1.3	153	3	US-09-732-560-86	Sequence 86, Appl	C 233	23	1.3	209	3	US-09-814-353-3605	Sequence 3605, Ap
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	C 162	23	1.3	156	3	US-09-814-353-5307	Sequence 5307, A	C 235	23	1.3	209	3	US-09-814-353-9919	Sequence 9919, Ap
	C 163	23	1.3	157	9	US-10-950-009-622	Sequence 622, App	C 236	23	1.3	209	8	US-09-814-353-12549	Sequence 12549, A
	C 164	23	1.3	160	3	US-09-732-560-113	Sequence 113, App	C 237	23	1.3	209	8	US-10-357-930-7946	Sequence 7946, Ap
	C 165	23	1.3	167	8	US-10-357-930-6085	Sequence 6085, Ap	C 238	23	1.3	210	3	US-09-814-353-18700	Sequence 18700, A
	C 166	23	1.3	167	8	US-10-357-930-37715	Sequence 37715, A	C 239	23	1.3	211	8	US-10-357-930-8217	Sequence 8217, Ap
	C 167	23	1.3	168	3	US-09-814-353-4256	Sequence 4256, Ap	C 240	23	1.3	211	8	US-10-357-930-37414	Sequence 37414, A
	C 168	23	1.3	168	3	US-09-814-353-10560	Sequence 10560, A	C 241	23	1.3	212	6	US-10-125-968-1417	Sequence 1417, Ap
	C 169	23	1.3	169	8	US-10-357-930-37554	Sequence 37554, A	C 242	23	1.3	212	9	US-10-950-009-958	Sequence 958, App

C 243	23	1.3	213	3	US-09-814-353-18481	Sequence 18481, A	C 316	23	1.3	266	8	US-10-357-930-45119	Sequence 45119, A
C 244	23	1.3	214	8	US-10-357-930-38041	Sequence 38041, A	C 317	23	1.3	267	8	US-10-357-930-37696	Sequence 37696, A
C 245	23	1.3	217	8	US-10-357-930-7368	Sequence 7368, A	C 318	23	1.3	267	8	US-10-357-930-37772	Sequence 37772, A
C 246	23	1.3	220	8	US-10-357-930-7328	Sequence 7328, A	C 319	23	1.3	268	3	US-09-814-353-6031	Sequence 6031, A
C 247	23	1.3	221	3	US-09-814-353-18201	Sequence 18201, A	C 320	23	1.3	268	3	US-09-814-353-12310	Sequence 12310, A
C 248	23	1.3	222	3	US-09-814-353-17728	Sequence 17728, A	C 321	23	1.3	268	8	US-10-357-930-38743	Sequence 38743, A
C 249	23	1.3	222	3	US-09-814-353-18350	Sequence 18350, A	C 322	23	1.3	269	8	US-10-357-930-8009	Sequence 8009, A
C 250	23	1.3	226	3	US-09-814-353-5530	Sequence 5530, A	C 323	23	1.3	271	3	US-09-814-353-4954	Sequence 4954, A
C 251	23	1.3	226	3	US-09-814-353-11817	Sequence 11817, A	C 324	23	1.3	271	3	US-09-814-353-11247	Sequence 11247, A
C 252	23	1.3	227	3	US-09-814-353-6041	Sequence 6041, A	C 325	23	1.3	271	3	US-09-814-353-11944	Sequence 11944, A
C 253	23	1.3	227	3	US-09-814-353-12320	Sequence 12320, A	C 326	23	1.3	272	3	US-09-814-353-5153	Sequence 5153, A
C 254	23	1.3	227	6	US-10-125-968-1238	Sequence 1238, A	C 327	23	1.3	272	3	US-09-814-353-5377	Sequence 5377, A
C 255	23	1.3	227	8	US-10-357-930-7987	Sequence 7987, A	C 328	23	1.3	272	3	US-08-814-353-11444	Sequence 11444, A
C 256	23	1.3	231	3	US-09-814-353-18092	Sequence 18092, A	C 329	23	1.3	272	3	US-09-814-353-11664	Sequence 11664, A
C 257	23	1.3	234	3	US-09-814-353-17216	Sequence 17216, A	C 330	23	1.3	273	3	US-09-814-353-5232	Sequence 5232, A
C 258	23	1.3	234	8	US-10-357-930-37410	Sequence 37410, A	C 331	23	1.3	273	3	US-09-814-353-11519	Sequence 11519, A
C 259	23	1.3	235	3	US-09-814-353-4764	Sequence 4764, A	C 332	23	1.3	273	5	US-10-060-036-4354	Sequence 4354, A
C 260	23	1.3	235	3	US-09-814-353-5885	Sequence 5885, A	C 333	23	1.3	276	3	US-09-732-560-40	Sequence 40, Appl
C 261	23	1.3	235	3	US-09-814-353-11061	Sequence 11061, A	C 334	23	1.3	277	8	US-10-357-930-37632	Sequence 37632, A
C 262	23	1.3	235	3	US-09-814-353-12166	Sequence 12166, A	C 335	23	1.3	277	8	US-10-357-930-37955	Sequence 37955, A
C 263	23	1.3	235	8	US-10-357-930-7559	Sequence 7559, A	C 336	23	1.3	278	9	US-10-950-009-158	Sequence 158, App
C 264	23	1.3	236	6	US-10-125-968-1262	Sequence 1262, A	C 337	23	1.3	278	3	US-09-969-034-22	Sequence 22, Appl
C 265	23	1.3	237	8	US-10-357-930-7525	Sequence 7525, A	C 338	23	1.3	279	3	US-09-814-353-6306	Sequence 6306, A
C 266	23	1.3	238	3	US-09-732-560-74	Sequence 74, Appl	C 339	23	1.3	279	3	US-09-814-353-12584	Sequence 12584, A
C 267	23	1.3	241	8	US-10-357-930-7977	Sequence 7977, A	C 340	23	1.3	279	3	US-09-814-353-17446	Sequence 17446, A
C 268	23	1.3	241	8	US-10-357-930-8241	Sequence 8241, A	C 341	23	1.3	280	7	US-10-357-930-7448	Sequence 7448, A
C 269	23	1.3	241	9	US-10-950-009-221	Sequence 221, App	C 342	23	1.3	280	8	US-10-663-561-165	Sequence 165, App
C 270	23	1.3	244	8	US-10-357-930-7837	Sequence 7837, A	C 343	23	1.3	281	8	US-10-357-930-35994	Sequence 35994, A
C 271	23	1.3	244	8	US-10-066-543-41	Sequence 41, Appl	C 344	23	1.3	282	3	US-09-814-353-4714	Sequence 4714, A
C 272	23	1.3	246	3	US-09-814-353-5423	Sequence 5423, A	C 345	23	1.3	282	3	US-09-814-353-5711	Sequence 5711, A
C 273	23	1.3	246	3	US-09-814-353-11710	Sequence 11710, A	C 346	23	1.3	282	3	US-09-814-353-11012	Sequence 11012, A
C 274	23	1.3	247	3	US-09-814-353-18754	Sequence 18754, A	C 347	23	1.3	282	3	US-09-814-353-11995	Sequence 11995, A
C 275	23	1.3	247	9	US-10-950-009-716	Sequence 716, App	C 348	23	1.3	282	8	US-10-357-930-8051	Sequence 8051, A
C 276	23	1.3	248	3	US-09-814-353-5058	Sequence 5058, A	C 349	23	1.3	283	3	US-09-814-353-2079	Sequence 2079, A
C 277	23	1.3	248	3	US-09-814-353-11350	Sequence 11350, A	C 350	23	1.3	283	3	US-09-814-353-8423	Sequence 8423, A
C 278	23	1.3	248	3	US-09-814-353-17941	Sequence 17941, A	C 351	23	1.3	283	3	US-09-814-353-17932	Sequence 17932, A
C 279	23	1.3	249	3	US-09-814-353-5815	Sequence 5815, A	C 352	23	1.3	284	6	US-10-125-968-1124	Sequence 1124, A
C 280	23	1.3	249	3	US-09-814-353-12097	Sequence 12097, A	C 353	23	1.3	284	6	US-10-125-968-1263	Sequence 1263, A
C 281	23	1.3	250	3	US-09-814-353-3331	Sequence 3331, A	C 354	23	1.3	285	8	US-10-723-860-1154	Sequence 1154, A
C 282	23	1.3	250	3	US-09-814-353-9652	Sequence 9652, A	C 355	23	1.3	285	8	US-10-357-930-37293	Sequence 37293, A
C 283	23	1.3	250	9	US-10-950-009-672	Sequence 672, App	C 356	23	1.3	285	9	US-10-950-009-824	Sequence 824, App
C 284	23	1.3	252	8	US-10-357-930-38132	Sequence 38132, A	C 357	23	1.3	285	9	US-10-756-149-1120	Sequence 1120, A
C 285	23	1.3	253	3	US-09-814-353-4885	Sequence 4885, A	C 358	23	1.3	287	3	US-09-814-353-5598	Sequence 5598, A
C 286	23	1.3	253	3	US-09-814-353-5270	Sequence 5270, A	C 359	23	1.3	287	3	US-09-814-353-6310	Sequence 6310, A
C 287	23	1.3	253	3	US-09-814-353-11181	Sequence 11181, A	C 360	23	1.3	287	3	US-09-814-353-11885	Sequence 11885, A
C 288	23	1.3	253	3	US-09-814-353-11557	Sequence 11557, A	C 361	23	1.3	287	3	US-09-814-353-12588	Sequence 12588, A
C 289	23	1.3	253	8	US-10-357-930-8172	Sequence 8172, A	C 362	23	1.3	287	9	US-10-950-009-31	Sequence 31, Appl
C 290	23	1.3	254	8	US-10-357-930-36011	Sequence 36011, A	C 363	23	1.3	288	3	US-09-732-560-6	Sequence 6, Appl
C 291	23	1.3	255	3	US-09-930-213-570	Sequence 570, App	C 364	23	1.3	288	3	US-09-814-353-17819	Sequence 17819, A
C 292	23	1.3	255	3	US-09-930-213-667	Sequence 667, App	C 365	23	1.3	289	3	US-09-814-353-4181	Sequence 4181, A
C 293	23	1.3	255	8	US-10-357-930-37790	Sequence 37790, A	C 366	23	1.3	289	3	US-09-814-353-10487	Sequence 10487, A
C 294	23	1.3	257	3	US-09-814-353-18625	Sequence 18625, A	C 367	23	1.3	289	3	US-09-814-353-17249	Sequence 17249, A
C 295	23	1.3	257	8	US-10-425-115-80930	Sequence 80930, A	C 368	23	1.3	289	9	US-10-950-009-231	Sequence 231, App
C 296	23	1.3	257	8	US-10-357-930-35960	Sequence 35960, A	C 369	23	1.3	290	8	US-10-357-930-6720	Sequence 6720, A
C 297	23	1.3	258	3	US-09-814-353-4717	Sequence 4717, A	C 370	23	1.3	291	8	US-10-425-115-141495	Sequence 141495, A
C 298	23	1.3	258	3	US-09-814-353-5260	Sequence 5260, A	C 371	23	1.3	291	8	US-10-357-930-37892	Sequence 37892, A
C 299	23	1.3	258	3	US-09-814-353-11015	Sequence 11015, A	C 372	23	1.3	292	8	US-10-357-930-7817	Sequence 7817, A
C 300	23	1.3	258	3	US-09-814-353-11547	Sequence 11547, A	C 373	23	1.3	292	8	US-09-814-353-4787	Sequence 4787, A
C 301	23	1.3	258	8	US-10-357-930-37330	Sequence 37330, A	C 374	23	1.3	293	3	US-09-814-353-11084	Sequence 11084, A
C 302	23	1.3	259	8	US-10-357-930-37636	Sequence 37636, A	C 375	23	1.3	293	3	US-09-732-560-118	Sequence 118, App
C 303	23	1.3	259	9	US-10-950-009-959	Sequence 959, App	C 376	23	1.3	295	3	US-09-814-353-5669	Sequence 5669, A
C 304	23	1.3	260	3	US-09-814-353-5564	Sequence 5564, A	C 377	23	1.3	295	3	US-09-814-353-11954	Sequence 11954, A
C 305	23	1.3	260	3	US-09-814-353-11851	Sequence 11851, A	C 378	23	1.3	295	6	US-10-125-968-1094	Sequence 1094, A
C 306	23	1.3	260	8	US-10-357-930-37385	Sequence 37385, A	C 379	23	1.3	296	3	US-09-814-353-4475	Sequence 4475, A
C 307	23	1.3	261	3	US-09-814-353-3841	Sequence 3841, A	C 380	23	1.3	296	3	US-09-814-353-5940	Sequence 5940, A
C 308	23	1.3	261	3	US-09-814-353-10150	Sequence 10150, A	C 381	23	1.3	296	3	US-09-814-353-10778	Sequence 10778, A
C 309	23	1.3	263	3	US-09-814-353-4636	Sequence 4636, A	C 382	23	1.3	296	3	US-09-814-353-12220	Sequence 12220, A
C 310	23	1.3	263	3	US-09-814-353-10935	Sequence 10935, A	C 383	23	1.3	297	3	US-09-814-353-18404	Sequence 18404, A
C 311	23	1.3	264	3	US-09-814-353-5108	Sequence 5108, A	C 384	23	1.3	297	8	US-10-357-930-6648	Sequence 6648, A
C 312	23	1.3	264	3	US-09-814-353-5826	Sequence 5826, A	C 385	23	1.3	298	3	US-09-814-353-3017	Sequence 3017, A
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C 314	23	1.3	264	3	US-09-814-353-12108	Sequence 12108, A	C 387	23	1.3	298	8	US-10-357-930-38068	Sequence 38068, A
C 315	23	1.3	266	8	US-10-357-930-36058	Sequence 36058, A	C 388	23	1.3	299	3	US-09-814-353-3301	Sequence 3301, A

C 389	23	1.3	299	3	US-09-814-353-3913	Sequence 3913, Ap
C 390	23	1.3	299	3	US-09-814-353-9622	Sequence 9622, Ap
C 391	23	1.3	299	3	US-09-814-353-10221	Sequence 10221, A
C 392	23	1.3	299	8	US-10-357-930-7675	Sequence 7675, Ap
C 393	23	1.3	300	3	US-09-814-353-5403	Sequence 5403, Ap
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C 395	23	1.3	300	3	US-09-814-353-12746	Sequence 12746, A
C 396	23	1.3	300	8	US-10-357-930-7819	Sequence 7819, Ap
C 397	23	1.3	301	3	US-09-814-353-3454	Sequence 3454, Ap
C 398	23	1.3	301	8	US-10-425-115-140765	Sequence 140765, A
C 399	23	1.3	302	8	US-10-357-930-7745	Sequence 7745, Ap
C 400	23	1.3	303	3	US-09-814-353-4270	Sequence 4270, Ap
C 401	23	1.3	303	3	US-09-814-353-10574	Sequence 10574, A
C 402	23	1.3	304	3	US-09-814-353-4918	Sequence 4918, Ap
C 403	23	1.3	304	3	US-09-814-353-11212	Sequence 11212, A
C 404	23	1.3	304	8	US-10-357-930-7356	Sequence 7356, Ap
C 405	23	1.3	304	8	US-10-357-930-37545	Sequence 37545, A
C 406	23	1.3	305	3	US-09-814-353-4252	Sequence 4252, Ap
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C 410	23	1.3	308	3	US-09-814-353-3733	Sequence 3733, Ap
C 411	23	1.3	308	3	US-09-814-353-10044	Sequence 10044, A
C 412	23	1.3	309	3	US-09-814-353-3152	Sequence 3152, Ap
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C 414	23	1.3	309	3	US-09-814-353-5601	Sequence 5601, Ap
C 415	23	1.3	309	3	US-09-814-353-9477	Sequence 9477, Ap
C 416	23	1.3	309	3	US-09-814-353-11571	Sequence 11571, A
C 417	23	1.3	309	3	US-09-814-353-11888	Sequence 11888, A
C 418	23	1.3	309	3	US-09-814-353-17157	Sequence 17157, A
C 419	23	1.3	310	3	US-09-732-560-52	Sequence 52, Appl
C 420	23	1.3	311	8	US-10-425-115-91139	Sequence 91139, A
C 421	23	1.3	311	9	US-10-950-009-43	Sequence 43, Appl
C 422	23	1.3	313	3	US-09-814-353-6071	Sequence 6071, Ap
C 423	23	1.3	313	3	US-09-814-353-12350	Sequence 12350, A
C 424	23	1.3	313	3	US-09-814-353-18398	Sequence 18398, A
C 425	23	1.3	314	3	US-09-814-353-6050	Sequence 6050, Ap
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C 435	23	1.3	317	3	US-09-732-560-50	Sequence 50, Appl
C 436	23	1.3	317	3	US-09-814-353-3060	Sequence 3060, Ap
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C 442	23	1.3	318	3	US-09-814-353-10835	Sequence 10835, A
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C 453	23	1.3	323	6	US-10-125-968-1376	Sequence 1376, Ap
C 454	23	1.3	324	3	US-09-814-353-4089	Sequence 4089, Ap
C 455	23	1.3	324	3	US-09-814-353-4662	Sequence 4662, Ap
C 456	23	1.3	324	3	US-09-814-353-5754	Sequence 5754, Ap
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C 465	23	1.3	325	3	US-09-814-353-4380	Sequence 4380, Ap
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C 467	23	1.3	326	3	US-09-814-353-4772	Sequence 4772, A
C 468	23	1.3	326	3	US-09-814-353-11069	Sequence 11069, A
C 469	23	1.3	326	3	US-09-814-353-16703	Sequence 16703, A
C 470	23	1.3	326	3	US-09-814-353-18362	Sequence 18362, A
C 471	23	1.3	327	3	US-09-814-353-3345	Sequence 3345, Ap
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C 473	23	1.3	327	3	US-09-814-353-9859	Sequence 9859, Ap
C 474	23	1.3	327	3	US-09-814-353-12198	Sequence 12198, A
C 475	23	1.3	327	3	US-09-814-353-17232	Sequence 17232, A
C 476	23	1.3	327	8	US-10-357-930-8158	Sequence 8158, Ap
C 477	23	1.3	327	8	US-10-357-930-18726	Sequence 18726, A
C 478	23	1.3	328	3	US-09-814-353-37973	Sequence 37973, A
C 479	23	1.3	328	8	US-10-357-930-37973	Sequence 37973, A
C 480	23	1.3	329	3	US-09-814-353-4341	Sequence 4341, Ap
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C 482	23	1.3	329	3	US-09-814-353-17483	Sequence 17483, A
C 483	23	1.3	329	8	US-10-357-930-7690	Sequence 7690, Ap
C 484	23	1.3	329	9	US-10-950-009-593	Sequence 593, App
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C 487	23	1.3	330	3	US-09-814-353-10919	Sequence 10919, A
C 488	23	1.3	330	3	US-09-814-353-11769	Sequence 11769, A
C 489	23	1.3	330	3	US-09-814-353-17646	Sequence 17646, A
C 490	23	1.3	330	3	US-09-814-353-18207	Sequence 18207, A
C 491	23	1.3	330	8	US-10-357-930-9103	Sequence 9103, Ap
C 492	23	1.3	331	3	US-09-814-353-4327	Sequence 4327, Ap
C 493	23	1.3	331	3	US-09-814-353-10631	Sequence 10631, A
C 494	23	1.3	332	3	US-09-814-353-3601	Sequence 3601, Ap
C 495	23	1.3	332	3	US-09-814-353-5594	Sequence 5594, Ap
C 496	23	1.3	332	3	US-09-814-353-9915	Sequence 9915, Ap
C 497	23	1.3	332	3	US-09-814-353-11881	Sequence 11881, A
C 498	23	1.3	333	3	US-09-814-353-4698	Sequence 4698, Ap
C 499	23	1.3	333	3	US-09-814-353-10997	Sequence 10997, A
C 500	23	1.3	333	3	US-09-814-353-16634	Sequence 16634, A

ALIGNMENTS

RESULT 1

US-09-989-890-105
; Sequence 105, Application US/09989890
; Publication No. US20040166105A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Pluta, Jason
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pro
; FILE REFERENCE: DEX-0287
; CURRENT APPLICATION NUMBER: US/09/989,890
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,509
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-890-105

Query Match 100.0%; Score 1713; DB 3; Length 1713;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCCGCTGGACACACCCCGCCAGCATCTGGGCTCCACGCTTGGACCGTGGAG 60
Db 1 ATGCCCCGCTGGACACACCCCGCCAGCATCTGGGCTCCACGCTTGGACCGTGGAG 60
QY 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACTCAGCCCCCACCACGCGC 120
Db 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACTCAGCCCCCACCACGCGC 120
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QY 181 ATCTCTGGCTCTGCTGAGCGCGCCCTTGGTTCCTCCACCTGCTGCTTGGCGACCC 240
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QY 301 CGCTGTGGAGCTGTGTGGGAGTGCAGCCCTGCTGTACTGAGGACTCCACTGAG 360
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RESULT 2
US-10-104-047-799
; Sequence 799, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 799
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-799

Query Match 93.1%; Score 1594; DB 6; Length 1785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCCCCGCGCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGACCGTGGAG 60
Db 90 ATGCCCCGCGCTGGACACCCCGCCAGCATCTGGGCTCCACGCTTGGAGCCGTGGAG 149
QY 61 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACCACTCAGCCCCCACCAGCCGC 120

Db 150 CGGCCAACAGAGCTATGTCTGGAGACATATGATAAACACACCTCAGCCCCCAACCAAGCGC 209
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Db 210 CGACCCGTAGACAGACCCCAAGACCCCTGGCACCATGGGCGAGAGCATTTACCTTC 269
Qy 181 ATCTCTGGGCTCTGTCTGAGCGCGCCCTTGAGTTCCTGAGTCCCCACCTGTCTGCTCTGGGCGACCC 240
Db 270 ATCTCTGGGCTCTGTCTGAGCGCGCCCTTGAGTTCCTGAGTCCCCACCTGTCTGCTCTGGGCGACCC 329
Qy 241 TGGGTGTGGAGTGTGTCGGGCTGCTTCTGCTTCCGCCGCTGCGGGGATTCCTCCAG 300
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Qy 301 CGCTGTGGAGCTGTGTGCGGGATGACAGCCCTGCTGTCTACTGAGAGCTCCACTGAG 360
Db 390 CGCTGTGGAGCTGTGTGCGGGATGACAGCCCTGCTGTCTACTGAGAGCTCCACTGAG 449
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Db 450 GGGACTGTGAAAGCCAACTGGGCAAGGAGCAATGGAGTGCCCCCAGGCCCTGTATCGT 509
Qy 421 GCACCCCCCAGCGGGGATGGCCAGCGGCTCAAGTCAACCATGGGCGAGAGCTTCAGC 480
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Qy 1081 ATCGCCCGAAGCTGAGGCTTATGAGCTCCAGGCTACCCAGAGCCATGACTCATCC 1140
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Qy 1681 CACAGTTGTAAAGTAC 1696
Db 1770 CACAGTTGTAAAGTAC 1785

RESULT 3
US-09-989-920-56
; Sequence 56, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989, 920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-56

Query Match 57.4%; Score 983; DB 3; Length 1977;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1103; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 598 CACAGCTGCCCAGACACCTTTGCCAGTAGTCTCTCGTGGCTCCGAGAGTACTATTCTTTC 657
Db 861 CACAGCTGCCCAGACACCTTTGCCAGTAGTCTCTCGTGGCTCCGAGAGTACTATTCTTTC 920
Qy 658 CATGAGTCCGACCTCGACCTGCCGAGATGGGAGTGGCGTCCATGTCGAGCCGAGAAAT 717

Db 921 CATGAGTCGACCTGGACCTGCCGAGATGGGAGTGGCTCCATGTCTGACGCCGAGAAATT 980
Qy 718 GATGTGCTCATCTTCAAGAGAGCTGACAGA-GCTGTTTCAGCGTACACAGATCGATGAGCT 776
Db 981 GATGTGCTCATCTTCAAGAGAGCTGACAGAGGCTGTTTCAGCGTACACAGATCGATGAGCT 1040
Qy 777 GGCNAGTGCATCATCAGACACTGTGTTCTTGGAGAACACAGTAAGATCTCGACCTTAT 836
Db 1041 GGCNAGTGCATCATCAGACACTGTGTTCTTGGAGAACACAGTAAGATCTCGACCTTAT 1100
Qy 837 CAGCAGCATCAGCAGGACTACCACTTGGATGAGCAGAGTGTGAGGCGCCCTGGTACG 896
Db 1101 CAGCAGCATCAGCAGGACTACCACTTGGATGAGCAGAGTGTGAGGCGCCCTGGTACG 1160
Qy 897 CGGCATCATTCGANTATAGTACCGAAAGAGCGGTGTCGCCCAAGACACTCGAGGGTGC 956
Db 1161 CGGCATCATTCGANTATAGTACCGAAAGAGCGGTGTCGCCCAAGACACTCGAGGGTGC 1220
Qy 957 TTCAACTCGGGCTGCTGCCCAACCGCTGTGCCCTGACAGTGGCCATGAGACCAATGT 1016
Db 1221 TTCAACTCGGGCTGCTGCCCAACCGCTGTGCCCTGACAGTGGCCATGAGACCAATGT 1280
Qy 1017 GGGCTCAGGTCCTCAGCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGA 1076
Db 1281 GGGCTCAGGTCCTCAGCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGA 1340
Qy 1077 TGCCATCGCCCGGAAGCTGAGGCTTATGAGGTCCTCAGGAGTCCAGCAAGCCATGACTC 1136
Db 1341 TGCCATCGCCCGGAAGCTGAGGCTTATGAGGTCCTCAGGAGTCCAGCAAGCCATGACTC 1400
Qy 1137 ATCCTTTCAGGGACCCGACACAGACTGCTGGGGGACCCCTTGTCTCAGGTGTACTGCTA 1196
Db 1401 ATCCTTTCAGGGACCCGACACAGACTGCTGGGGGACCCCTTGTCTCAGGTGTACTGCTA 1460
Qy 1197 ACCCTTGCAGGGACCCGACACAGACTGCTGGGGGACCCCTTGTCTCAGGTGTACTGCTA 1256
Db 1461 ACCCTTGCAGGGACCCGACACAGACTGCTGGGGGACCCCTTGTCTCAGGTGTACTGCTA 1520
Qy 1257 AGGGGACCCAGGAACCCCTGTGGGAGAGGCTTACAGCTGAGCAGTGCACACTCTGGCTC 1316
Db 1521 AGGGGACCCAGGAACCCCTGTGGGAGAGGCTTACAGCTGAGCAGTGCACACTCTGGCTC 1580
Qy 1317 CTCTGCTTGGCTGACTGGGTTCTTGGACATGTGCAATTTCACTGGGCCATGGGATCTA 1376
Db 1581 CTCTGCTTGGCTGACTGGGTTCTTGGACATGTGCAATTTCACTGGGCCATGGGATCTA 1640
Qy 1377 CATCTCTTGCATCCCGAGCTGGTCTGATCCCTGCGAGGCGCCCTTCTCTGCTCATG 1436
Db 1641 CATCTCTTGCATCCCGAGCTGGTCTGATCCCTGCGAGGCGCCCTTCTCTGCTCATG 1700
Qy 1437 GTCTTCAGGTGGCTGATCATGGAAGTAAAGGATTAAGGCATTAACCTTCTGGGAGTGAAC 1496
Db 1701 GTCTTCAGGTGGCTGATCATGGAAGTAAAGGATTAAGGCATTAACCTTCTGGGAGTGAAC 1760
Qy 1497 CTTGACTCATCCCTTATTTGGCAACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGG 1556
Db 1761 CTTGACTCATCCCTTATTTGGCAACCTTAACCAATCATGCAAACTTCTCCCTCCCTGGGG 1820
Qy 1557 TAATTCAACAGTTAAAGAGCTTATCTTAAATGATTTGTTGGGGGGTGGGACGGCC 1616
Db 1821 TAATTCAACAGTTAAAGAGCTTATCTTAAATGATTTGTTGGGGGGTGGGACGGCC 1880
Qy 1617 CACTCTATGTTATGTTAAGGATTTGGTCTTGGTCTTGGCTGATGTTCTGATCTTAAACA 1676
Db 1881 CACTCTATGTTATGTTAAGGATTTGGTCTTGGTCTTGGCTGATGTTCTGATCTTAAACA 1940
Qy 1677 TGACCACAGTTTGTAAAGTAACTCTCG 1700
Db 1941 TGACCACAGTTTGTAAAGTAACTCTCG 1964

; Sequence 117, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-117

Query Match 57.4%; Score 983; DB 3; Length 1977;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1103; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 598 CACAGCCTGCCAGCACCTTTGCCAGTAGTCTCTGGTCTCCGAGGAGTACTATTCTTTC 657
Db 861 CACAGCCTGCCAGCACCTTTGCCAGTAGTCTCTGGTCTCCGAGGAGTACTATTCTTTC 920
Qy 658 CATGAGTCGGACCTGACACCTGCCGAGATGGGAGTGGCTCCATGTCCAGCCGAGAAATT 717
Db 921 CATGAGTCGGACCTGACACCTGCCGAGATGGGAGTGGCTCCATGTCCAGCCGAGAAATT 980
Qy 718 GATGTGCTCATCTTCAAGAGAGCTGACAGA-GCTGTTTCAGCGTACACAGATCGATGAGCT 776
Db 981 GATGTGCTCATCTTCAAGAGAGCTGACAGAGGCTGTTTCAGCGTACACAGATCGATGAGCT 1040
Qy 777 GGCNAGTGCATCATCAGACACTGTGTTCTTGGAGAACACAGTAAGATCTCGACCTTAT 836
Db 1041 GGCNAGTGCATCATCAGACACTGTGTTCTTGGAGAACACAGTAAGATCTCGACCTTAT 1100
Qy 837 CAGCAGCATCAGCAGGACTACCACTTGGATGAGCAGAGTGTGAGGCGCCCTGGTACG 896
Db 1101 CAGCAGCATCAGCAGGACTACCACTTGGATGAGCAGAGTGTGAGGCGCCCTGGTACG 1160
Qy 897 CGGCATCATTCGANTATAGTACCGAAAGAGCGGTGTCGCCCAAGACACTCGAGGGTGC 956
Db 1161 CGGCATCATTCGANTATAGTACCGAAAGAGCGGTGTCGCCCAAGACACTCGAGGGTGC 1220
Qy 957 TTCAACTCGGGCTGCTGCCCAACCGCTGTGCCCTGACAGTGGCCATGAGACCAATGT 1016
Db 1221 TTCAACTCGGGCTGCTGCCCAACCGCTGTGCCCTGACAGTGGCCATGAGACCAATGT 1280
Qy 1017 GGGCTCAGGTCCTCAGCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGA 1076
Db 1281 GGGCTCAGGTCCTCAGCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGACTGCAGA 1340
Qy 1077 TGCCATCGCCCGGAAGCTGAGGCTTATGAGGTCCTCAGGAGTCCAGCAAGCCATGACTC 1136
Db 1341 TGCCATCGCCCGGAAGCTGAGGCTTATGAGGTCCTCAGGAGTCCAGCAAGCCATGACTC 1400
Qy 1137 ATCCTTTCAGGGACCCGACACAGACTGCTGGGGGACCCCTTGTCTCAGGTGTACTGCTA 1196
Db 1401 ATCCTTTCAGGGACCCGACACAGACTGCTGGGGGACCCCTTGTCTCAGGTGTACTGCTA 1460
Qy 1197 ACCCTTGCAGGGACCCGACACAGACTGCTGGGGGACCCCTTGTCTCAGGTGTACTGCTA 1256
Db 1461 ACCCTTGCAGGGACCCGACACAGACTGCTGGGGGACCCCTTGTCTCAGGTGTACTGCTA 1520
Qy 1257 AGGGGACCCAGGAACCCCTGTGGGAGAGGCTTACAGCTGAGCAGTGCACACTCTGGCTC 1316
Db 1521 AGGGGACCCAGGAACCCCTGTGGGAGAGGCTTACAGCTGAGCAGTGCACACTCTGGCTC 1580


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; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 12051
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-12051
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Query Match      18.7%; Score 321; DB 9; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.6e-160;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCGCGCTGAGACACCCCGCCAGCATCTGGGCTCCACGCTTGGAGCCGTGGAG 60
DB 80 ATGCCCGCGCTGAGACACCCCGCCAGCATCTGGGCTCCACGCTTGGAGCCGTGGAG 139

QY 61 CGGCCAACAGAGATATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGCCGC 120
DB 140 CGGCCAACAGAGATATGTCTGGAGACATATGATAAACACCTCAGCCCCCACCAGCCGC 199

QY 121 CGCACCGGTAGACACACCCAGGACCTTGGCCACCATGAGCCAGAGAGCATTACCTTC 180
DB 200 CGCACCGGTAGACACACCCAGGACCTTGGCCACCATGAGCCAGAGAGCATTACCTTC 259

QY 181 ATCTCTGGCTCTGCTGAGCGCGGCTTGAGTCCCGCCACCTGCTGCTGCTGCGGACCC 240
DB 260 ATCTCTGGCTCTGCTGAGCGCGGCTTGAGTCCCGCCACCTGCTGCTGCTGCGGACCC 319

QY 241 TGGGTGTGGAGTGTGTCGGGCTGCTGCTTCCGCGCTGCGCGGATTCCTCCAG 300
DB 320 TGGGTGTGGAGTGTGTCGGGCTGCTGCTTCCGCGCTGCGCGGATTCCTCCAG 379

QY 301 CGCTGTGGAGCCTGTGTGGG 321
DB 380 CGCTGTGGAGCCTGTGTGGG 400
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RESULT 10
US-10-779-543-1705
; Sequence 1705, Application US/10779543
; Publication No. US2005027917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: US/10/779, 543
; PRIOR FILING DATE: 2002-02-15
```

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; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1705
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-779-543-1705

Query Match      17.5%; Score 300; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 6.1e-149;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 825 CTCGGACCTTATCAGCAGCATCAGCAGGATCAGCAGGATACCACTGGATGACGAGGATGCTCAGGG 884
DB 1 CTCGGACCTTATCAGCAGCATCAGCAGGATCAGCAGGATACCACTGGATGACGAGGATGCTCAGGG 60

QY 885 CCGCCTGGTACGCGGCATCATTCGCATTAGTATACCGAAAGAGCCGTGCTCGCCACAGAC 944
DB 61 CCGCCTGGTACGCGGCATCATTCGCATTAGTATACCGAAAGAGCCGTGCTCGCCACAGAC 120

QY 945 CTCGGAGGCTGTTCAACTCGGGCTGCTGCCCGAACCGCTGCTGCCCTGACAGTGGCCA 1004
DB 121 CTCGGAGGCTGTTCAACTCGGGCTGCTGCCCGAACCGCTGCTGCCCTGACAGTGGCCA 180

QY 1005 TGAGACCATGTTGGGCTCAGGCTCAGCCAGAGATGAGCTGACAGTGCAGATCTCCAGGA 1064
DB 181 TGAGACCATGTTGGGCTCAGGCTCAGCCAGAGATGAGCTGACAGTGCAGATCTCCAGGA 240

QY 1065 GACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCTTATGGAGCTTCCAGGTTACCCAGC 1124
DB 241 GACGACTGCAGATGCCATCGCCCGGAAGCTGAGGCTTATGGAGCTTCCAGGTTACCCAGC 300

RESULT 11
US-10-076-555-34
; Sequence 34, Application US/10076555
; Publication No. US20030065156A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kaseam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
```

```
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Novel Human Genes and Gene Expression
; TITLE OF INVENTION: Products I
; FILE REFERENCE: 2300-1480
; CURRENT APPLICATION NUMBER: US/10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,877
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-555-34

Query Match 14.5%; Score 249; DB 5; Length 300;
Best Local Similarity 99.7%; Pred. No. 1e-121;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGACAGAGCTGTTTCAGCGTACACAGATCGATGAGCTGGCCAAAGTGCACATCAGACACTG 799
Db 1 TGACAGAGCTGTTTCAGCGTACACAGATCGATGAGCTGGCCAAAGTGCACATCAGACACTG 60

QY 800 TGTTCTCGGAGAGACAGTAAGATCTCGACCTTATCAGCAGCATCAGCAGGACTACC 859
Db 61 TGTTCTCGGAGAGACAGTAAGATCTCGACCTTATCAGCAGCATCAGCAGGACTACC 120

QY 860 ACCTGATGAGCAGGAGTGTGAGGGCGGCTGTGACGGGCATCTTCGATTAGTACC 919
Db 121 ACCTGATGAGCAGGAGTGTGAGGGCGGCTGTGACGGGCATCTTCGATTAGTACC 180

QY 920 GAAAGAGCGGTGCTCGCCACAGACCTCGAGAGGCTGTTCAACTCGGGCTGCTGCCCAA 979
Db 181 GAAAGAGCGGTGCTCGCCACAGACCTCGAGAGGCTGTTCAACTCGGGCTGCTGCCCAA 240

QY 980 CCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGCTTCAGCCAGGATG 1039
Db 241 CCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGCTTCAGCCAGGATG 300

RESULT 12
US-10-779-543-34
; Sequence 34, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03

; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Novel Human Genes and Gene Expression
; TITLE OF INVENTION: Products I
; FILE REFERENCE: 2300-1480
; CURRENT APPLICATION NUMBER: US/10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/105,877
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-555-34

Query Match 14.5%; Score 249; DB 9; Length 300;
Best Local Similarity 99.7%; Pred. No. 1e-121;
Matches 299; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 740 TGACAGAGCTGTTTCAGCGTACACAGATCGATGAGCTGGCCAAAGTGCACATCAGACACTG 799
Db 1 TGACAGAGCTGTTTCAGCGTACACAGATCGATGAGCTGGCCAAAGTGCACATCAGACACTG 60

QY 800 TGTTCTCGGAGAGACAGTAAGATCTCGACCTTATCAGCAGCATCAGCAGGACTACC 859
Db 61 TGTTCTCGGAGAGACAGTAAGATCTCGACCTTATCAGCAGCATCAGCAGGACTACC 120

QY 860 ACCTGATGAGCAGGAGTGTGAGGGCGGCTGTGACGGGCATCTTCGATTAGTACC 919
Db 121 ACCTGATGAGCAGGAGTGTGAGGGCGGCTGTGACGGGCATCTTCGATTAGTACC 180

QY 920 GAAAGAGCGGTGCTCGCCACAGACCTCGAGAGGCTGTTCAACTCGGGCTGCTGCCCAA 979
Db 181 GAAAGAGCGGTGCTCGCCACAGACCTCGAGAGGCTGTTCAACTCGGGCTGCTGCCCAA 240

QY 980 CCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGCTTCAGCCAGGATG 1039
Db 241 CCGCTGCTGCCCTGACAGTGGCCATGAGACCATGTTGGGCTCAGGCTTCAGCCAGGATG 300

RESULT 13
US-10-074-475-124
; Sequence 124, Application US/10074475
; Publication No. US20030092898A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
; FILE REFERENCE: DEX-0313
; FILE REFERENCE: DEX-0313
; CURRENT APPLICATION NUMBER: US/10/074,475
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,292
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-074-475-124
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Query Match 13.0%; Score 222; DB 5; Length 654;
Best Local Similarity 100.0%; Pred. No. 2.5e-107;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 ATGATTAACACCTCAGCCGCCACCAAGCGCGGACCCGTAGACAGACCCCAAGGACC 148
|||||
Db 1 ATGATTAACACCTCAGCCGCCACCAAGCGCGGACCCGTAGACAGACCCCAAGGACC 60
|||||

QY 149 CTGGCCACCATGGCCGAGAGACATTCATCTCTGCTCTGCTGAGCGGCCCTTG 208
|||||
Db 61 CTGGCCACCATGGCCGAGAGACATTCATCTCTGCTCTGCTGAGCGGCCCTTG 120
|||||

QY 209 AGTCCCGCCACCTGCTGCTGCTGCGGACCTGCGGTGTGGAGTGGTGCCTGGCT 268
|||||
Db 121 AGTCCCGCCACCTGCTGCTGCTGCGGACCTGCGGTGTGGAGTGGTGCCTGGCT 180
|||||

QY 269 TCTGCTTCGCGCGCTGCGGGATTGCTTCAGCGCTGTGGAG 310
|||||
Db 181 TCTGCTTCGCGCGCTGCGGGATTGCTTCAGCGCTGTGGAG 222
|||||

RESULT 14
US-09-989-920-116/c
; Sequence 116, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prob
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 116
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-116

Query Match 7.0%; Score 120; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 8.2e-53;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 AAGCTTATCTTAATGATGTTATTTGGGGTGGCGAGGCCACCTATGTTATGTTAA 1634
|||||
Db 120 AAGCTTATCTTAATGATGTTATTTGGGGTGGCGAGGCCACCTATGTTATGTTAA 61
|||||

QY 1635 GGAGTTGGTTCTGGTTCTGGCTGATGTTCTGTATCTTAACATGACCAAGTTTGAAGT 1694
|||||
Db 60 GGAGTTGGTTCTGGTTCTGGCTGATGTTCTGTATCTTAACATGACCAAGTTTGAAGT 1

RESULT 15
US-10-779-543-5731
; Sequence 5731, Application US/10779543
; Publication No. US2005022791A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471

; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5731
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 15, 16, 17, 18, 20,
; LOCATION: 22, 23, 24, 25, 28, 29, 30, 36, 41, 85, 89, 97, 106, 108,
; LOCATION: 115, 134, 139, 177, 185, 207, 232, 275, 283, 303, 320, 327,
; LOCATION: 356, 414, 451, 469, 551, 566, 582, 588, 591, 605, 631, 656
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 661, 678, 681, 687, 689, 702, 706, 710, 711, 713, 722
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-5731

Query Match 2.2%; Score 38; DB 9; Length 728;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1218 CACACCCCTTCTGGGAGAGCATGGCCTACAGATGAA 1255
|||||
Db 487 CACACCCCTTCTGGGAGAGCATGGCCTACAGATGAA 524
|||||

RESULT 16
US-11-036-317-669570
; Sequence 669570, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 669570
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-669570

Query Match 1.5%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 GATGTTAAGCTCAAGGCTCCCTG 511
|||||

```
Db      1  GATGTTAAGCTCAAAGGCATCCCTG 25

RESULT 17
US-10-131-827-8473
; Sequence 8473, Application US/10131827
; Publication No. US2004009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8473
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(224)
; OTHER INFORMATION: n = A, C, T or G
US-10-131-827-8473

Query Match      1.5%; Score 25; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1689  GTAAGTACCTCGCGCGGACACGC 1713
Db      189  GTAAGTACCTCGCGCGGACACGC 213

RESULT 18
US-10-357-930-37484/c
; Sequence 37484, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37484

US-09-989-890-105.oligo.rnpbm
```

```
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-37484

Query Match      1.5%; Score 25; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1689  GTAAGTACCTCGCGCGGACACGC 1713
Db      97  GTAAGTACCTCGCGCGGACACGC 73

RESULT 19
US-09-814-353-17410/c
; Sequence 17410, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17410
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-17410

Query Match      1.5%; Score 25; DB 3; Length 275;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1689  GTAAGTACCTCGCGCGGACACGC 1713
Db      87  GTAAGTACCTCGCGCGGACACGC 63

RESULT 20
US-10-357-930-7524/c
; Sequence 7524, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
```

; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7524
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 123, 131, 149, 152, 166, 201, 284
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-7524

Query Match 1.5%; Score 25; DB 8; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACACGC 1713
Db 39 GTAAGTACCTCGCGCGGACACGC 15

RESULT 21

US-09-814-353-5095
; Sequence 5095, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5095
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-5095

Query Match 1.5%; Score 25; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACACGC 1713

Db 280 GTAAGTACCTCGCGCGGACACGC 304

RESULT 22

US-09-814-353-11387
; Sequence 11387, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11387
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-11387

Query Match 1.5%; Score 25; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACACGC 1713
Db 280 GTAAGTACCTCGCGCGGACACGC 304

RESULT 23

US-10-060-036-4393
; Sequence 4393, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4393
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-4393

Query Match 1.5%; Score 25; DB 5; Length 453;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1689 GTAAGTACCTCGCGCGGACACGC 1713
Db 428 GTAAGTACCTCGCGCGGACACGC 452

RESULT 24
US-09-814-353-17771
; Sequence 17771, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17771
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-17771

Query Match 1.5%; Score 25; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACACGC 1713
Db 351 GTAAGTACCTCGCGCGGACACGC 375

RESULT 25
US-10-074-511-10/c
; Sequence 10, Application US/10074511
; Publication No. US20030176672A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Caferkey, Robert
; APPLICANT: Liu, Chenghua
; APPLICANT: Sun, Yongming
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Ph
; FILE REFERENCE: DEX-0314
; CURRENT APPLICATION NUMBER: US/10/074,511
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,289
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 810
; TYPE: DNA
```

```
; ORGANISM: Homo sapien
US-10-074-511-10

Query Match 1.5%; Score 25; DB 6; Length 810;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACACGC 1713
Db 25 GTAAGTACCTCGCGCGGACACGC 1

RESULT 26
US-10-198-846-5605/c
; Sequence 5605, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5605
; LENGTH: 1252
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 3, 4, 5, 14, 18, 19, 20, 22, 26, 28, 29, 35, 36, 42, 46,
; LOCATION: 48, 50, 51, 52, 57, 58, 60, 62, 63, 64, 77, 81, 83, 90,
; LOCATION: 93, 96, 99, 102, 103, 107, 115, 116, 121, 124, 127, 146,
; LOCATION: 169, 382, 433, 437, 465, 473, 480, 498, 517, 539, 541, 572
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 577, 591, 610, 627, 628, 657, 664, 672, 709, 712, 720, 726,
; LOCATION: 732, 734, 738, 753, 756, 772, 783, 789, 790, 797, 813, 814,
; LOCATION: 815, 830, 835, 837, 846, 864, 868, 873, 877, 896, 903, 921,
; LOCATION: 925, 926, 928, 936, 941, 957, 958, 974, 980, 985, 986
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 991, 996, 997, 999, 1001, 1002, 1008, 1010, 1015, 1018, 1019,
; LOCATION: 1025, 1029, 1031, 1039, 1040, 1046, 1048, 1054, 1055, 1059,
; LOCATION: 1060, 1063, 1067, 1068, 1069, 1070, 1072, 1075, 1079, 1080,
; LOCATION: 1085, 1091, 1094, 1097, 1100, 1102, 1105, 1107, 1116
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1126, 1128, 1132, 1137, 1138, 1140, 1141, 1144, 1148, 1151,
; LOCATION: 1156, 1165, 1166, 1173, 1176, 1183, 1188, 1193, 1194, 1195,
; LOCATION: 1199, 1201, 1209, 1212, 1215, 1216, 1220, 1221, 1222, 1223,
; LOCATION: 1224, 1230, 1231, 1239, 1240, 1243, 1244, 1245, 1252
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-5605

Query Match 1.5%; Score 25; DB 5; Length 1252;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1689 GTAAGTACCTCGCGCGGACACGC 1713
Db 224 GTAAGTACCTCGCGCGGACACGC 200
```

```
RESULT 27
US-10-950-009-1051/c
; Sequence 1051, Application US/10950009
; Publication No. US20050069934A1
; GENERAL INFORMATION:
; APPLICANT: BERKA, Randy
; APPLICANT: BASHKIROVA, Elena
; APPLICANT: REY, Michael
; TITLE OF INVENTION: Methods For Monitoring Gene Expression
; FILE REFERENCE: 10541.200-US
; PRIOR APPLICATION NUMBER: US/10/950,009
; CURRENT FILING DATE: 2004-09-24
; PRIOR FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: 60/506,140
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 1190
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1051
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Trichoderma reesei
US-10-950-009-1051

Query Match      1.4%; Score 24; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
Db 24 TAAGTACCTCGCGCGACACGC 1

RESULT 28
US-10-477-445-15
; Sequence 15, Application US/10477445
; Publication No. US20050130138A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: Immune-related proteins and the regulation of the same
; FILE REFERENCE: RCK-12
; CURRENT APPLICATION NUMBER: US/10/477,445
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: PCT/EP02/05127
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/290,312
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 111
; SEQ ID NO 15
; LENGTH: 232
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 145..145
; OTHER INFORMATION: unknown nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 231..231
; OTHER INFORMATION: unknown nucleotide
US-10-477-445-15

Query Match      1.4%; Score 24; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TGTAACTACTCGCGCGACACGC 1711
Db 207 TGTAACTACTCGCGCGACACGC 230

RESULT 29
US-09-814-353-17222/c
; Sequence 17222, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17222
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-17222

Query Match      1.4%; Score 24; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
Db 77 TAAGTACCTCGCGCGACACGC 54

RESULT 30
US-09-814-353-5345/c
; Sequence 5345, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5345
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-5345
```

Query Match 1.4%; Score 24; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 31

US-09-814-353-11632/c
; Sequence 11632, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11632
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-814-353-11632

Query Match 1.4%; Score 24; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 32

US-09-814-353-16395/c
; Sequence 16395, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16395
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-16395

Query Match 1.4%; Score 24; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 54 TAAGTACCTCGCGCGGACACGC 31

RESULT 33

US-09-814-353-3678/c
; Sequence 3678, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3678
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-814-353-3678

Query Match 1.4%; Score 24; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 34

US-09-814-353-9991/c
; Sequence 9991, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela


```
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9991
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-9991

Query Match          1.4%; Score 24; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
DB 30 TAAGTACCTCGCGCGACACGC 7

RESULT 35
US-09-814-353-4074/c
; Sequence 4074, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4074
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-4074

Query Match          1.4%; Score 24; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1690 TAAGTACCTCGCGCGACACGC 1713
DB 30 TAAGTACCTCGCGCGACACGC 7

RESULT 36
US-09-814-353-10381/c
; Sequence 10381, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10381
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-10381

Query Match          1.4%; Score 24; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
DB 30 TAAGTACCTCGCGCGACACGC 7

RESULT 37
US-09-814-353-2976/c
; Sequence 2976, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
```

; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2976
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 181, 183, 191, 314
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-2976

Query Match 1.4%; Score 24; DB 3; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGGCACACGC 1713
|||||
DB 30 TAAGTACCTCGCGGCACACGC 7

RESULT 38

US-09-814-353-9305/c
; Sequence 9305, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9305
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 181, 183, 191, 314
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9305

Query Match 1.4%; Score 24; DB 3; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGGCACACGC 1713
|||||
DB 30 TAAGTACCTCGCGGCACACGC 7

RESULT 39

US-09-969-034-1870
; Sequence 1870, Application US/09969034

; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1870
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 259
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-1870

Query Match 1.4%; Score 24; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGGCACACGC 1713
|||||
DB 289 TAAGTACCTCGCGGCACACGC 312

RESULT 40

US-09-814-353-17947/c
; Sequence 17947, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17947
; LENGTH: 326
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 114

```
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-17947

Query Match      1.4%; Score 24; DB 3; Length 326;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 113 TAAGTACCTCGCGCGGACACGC 90

RESULT 41
US-10-357-930-7995/c
; Sequence 7995, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7995
; LENGTH: 346
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-7995

Query Match      1.4%; Score 24; DB 8; Length 346;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 42
US-09-814-353-4711/c
; Sequence 4711, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11010
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 204
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11010

Query Match      1.4%; Score 24; DB 3; Length 368;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4711

Query Match      1.4%; Score 24; DB 3; Length 368;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4711
```

```
QY 1690 TAAGTACCTCGCGCGACACGC 1713
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 44
US-09-814-353-5958/c
; Sequence 5958, Application US/09814353
; Publication No. US2003016581A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5958
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: 236, 252, 254, 313, 322, 329
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-5958

Query Match 1.4%; Score 24; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-814-353-5958
QY 1690 TAAGTACCTCGCGCGACACGC 1713
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 45
US-09-814-353-12238/c
; Sequence 12238, Application US/09814353
; Publication No. US2003016581A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5958
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: 236, 252, 254, 313, 322, 329
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-5958

Query Match 1.4%; Score 24; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-814-353-5958
QY 1690 TAAGTACCTCGCGCGACACGC 1713
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 46
US-10-357-930-6066/c
; Sequence 6066, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6066
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-6066

Query Match 1.4%; Score 24; DB 8; Length 376;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-814-353-16765/c
RESULT 47
US-09-814-353-16765/c
```

```
QY 1690 TAAGTACCTCGCGCGACACGC 1713
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 46
US-10-357-930-6066/c
; Sequence 6066, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6066
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-6066

Query Match 1.4%; Score 24; DB 8; Length 376;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-814-353-12238
QY 1690 TAAGTACCTCGCGCGACACGC 1713
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 47
US-09-814-353-16765/c
```

```
; Sequence 16765, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16765
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-16765

Query Match          1.4%; Score 24; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 101 TAAGTACCTCGCGCGGACACGC 78

RESULT 48
US-09-814-353-2902/c
; Sequence 2902, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2902
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-09-814-353-2902

Query Match          1.4%; Score 24; DB 3; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 49
US-09-814-353-9231/c
; Sequence 9231, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9231
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-9231

Query Match          1.4%; Score 24; DB 3; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 50
US-09-814-353-16375/c
; Sequence 16375, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16375
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16375
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-16375

Query Match      1.4%; Score 24; DB 3; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
Db 110 TAAGTACCTCGCGCGACACGC 87

RESULT 51
US-09-814-353-3267/c
; Sequence 3267, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9592
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 327, 378, 384
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9592

Query Match      1.4%; Score 24; DB 3; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACACGC 1713
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 53
US-10-357-930-8043/c
; Sequence 8043, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
```

```
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8043
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 37, 54, 147
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-8043

Query Match
Best Local Similarity 1.4%; Score 24; DB 8; Length 404;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 54
US-09-814-353-16049/c
; Sequence 16049, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16049
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-16049

Query Match
Best Local Similarity 1.4%; Score 24; DB 3; Length 409;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 111 TAAGTACCTCGCGCGGACACGC 88

RESULT 55
US-09-814-353-17159/c
; Sequence 17159, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
```

```
Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 57
US-09-814-353-11508/c
; Sequence 11508, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11508
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 271
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11508

Query Match 1.4%; Score 24; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 58
US-09-814-353-12779
; Sequence 12779, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15689
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-15689

Query Match 1.4%; Score 24; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 391 TAAGTACCTCGCGCGGACACGC 414

RESULT 59
US-09-814-353-15689/c
; Sequence 15689, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15689
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-15689

Query Match 1.4%; Score 24; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 111 TAAGTACCTCGCGCGGACACGC 88

RESULT 60
US-09-814-353-5813
; Sequence 5813, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
```



```
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5813
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-5813

Query Match      1.4%; Score 24; DB 3; Length 421;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
DB 391 TAAGTACCTCGGCGGACACGC 414
|||||
; US-10-357-930-39249/c
RESULT 61
US-10-357-930-39249/c
; Sequence 39249, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39249
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-357-930-39249
```

```
Query Match      1.4%; Score 24; DB 8; Length 424;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
DB 85 TAAGTACCTCGGCGGACACGC 62
|||||
RESULT 62
US-10-198-846-7580/c
; Sequence 7580, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7580
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 384
; OTHER INFORMATION: n = A,T,C or G
; US-10-198-846-7580
```

```
Query Match      1.4%; Score 24; DB 5; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
DB 105 TAAGTACCTCGGCGGACACGC 82
|||||
RESULT 63
US-09-814-353-18496/c
; Sequence 18496, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
```

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; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18496
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-18496

Query Match      1.4%; Score 24; DB 3; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACCAACGC 1713
Db 111 TAAGTACCTCGCGCGACCAACGC 88

RESULT 64
US-10-357-930-6566/c
; Sequence 6566, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6566
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-6566

Query Match      1.4%; Score 24; DB 8; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACCAACGC 1713
Db 30 TAAGTACCTCGCGCGACCAACGC 7

RESULT 65
US-09-814-353-18622/c
; Sequence 18622, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
```

```
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18622
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-18622

Query Match      1.4%; Score 24; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGACCAACGC 1713
Db 95 TAAGTACCTCGCGCGACCAACGC 72

RESULT 66
US-10-357-930-37944/c
; Sequence 37944, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37944
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-37944

Query Match      1.4%; Score 24; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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OY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 56 TAAGTACCTCGCGCGACACGC 33

RESULT 67
US-09-814-353-3100/c
; Sequence 3100, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3100
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: 182, 223, 225, 281, 285, 392
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-3100

Query Match 1.4%; Score 24; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 68
US-09-814-353-9426/c
; Sequence 9426, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9426
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: 182, 223, 225, 281, 285, 392
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9426

Query Match 1.4%; Score 24; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 69
US-09-814-353-18016/c
; Sequence 18016, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18016
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: 182, 223, 225, 281, 285, 392
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-18016

Query Match 1.4%; Score 24; DB 3; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 106 TAAGTACCTCGCGCGACACGC 83

RESULT 70
US-09-814-353-15845/c
; Sequence 15845, Application US/09814353
; Publication No. US20030165831A1
```

```
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9426
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: 182, 223, 225, 281, 285, 392
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9426

Query Match 1.4%; Score 24; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACCTCGCGCGACACGC 7

RESULT 69
US-09-814-353-18016/c
; Sequence 18016, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18016
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: 182, 223, 225, 281, 285, 392
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-18016

Query Match 1.4%; Score 24; DB 3; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 106 TAAGTACCTCGCGCGACACGC 83

RESULT 70
US-09-814-353-15845/c
; Sequence 15845, Application US/09814353
; Publication No. US20030165831A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15845
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-15845

Query Match          1.4%; Score 24; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCAACGC 1713
Db 73 TAAGTACCTCGCGCGGACCAACGC 50

RESULT 71
US-09-814-353-4306/c
; Sequence 4306, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4306
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature

Query Match          1.4%; Score 24; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCAACGC 1713
Db 73 TAAGTACCTCGCGCGGACCAACGC 50

RESULT 72
US-09-814-353-10610/c
; Sequence 10610, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10610
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature

Query Match          1.4%; Score 24; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCAACGC 1713
Db 73 TAAGTACCTCGCGCGGACCAACGC 50

RESULT 73
US-10-357-930-36059/c
; Sequence 36059, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
```

```
; LOCATION: 324
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4306

Query Match          1.4%; Score 24; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCAACGC 1713
Db 30 TAAGTACCTCGCGCGGACCAACGC 7

RESULT 72
US-09-814-353-10610/c
; Sequence 10610, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10610
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature

Query Match          1.4%; Score 24; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACCAACGC 1713
Db 30 TAAGTACCTCGCGCGGACCAACGC 7

RESULT 73
US-10-357-930-36059/c
; Sequence 36059, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
```

```
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36059
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-36059

Query Match      1.4%; Score 24; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 101 TAAGTACCTCGCGCGGACACGC 78

RESULT 74
US-10-357-930-37991/c
; Sequence 37991, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37991
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-37991

Query Match      1.4%; Score 24; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 101 TAAGTACCTCGCGCGGACACGC 78

US-10-001-857-66/c
; Sequence 66, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-857-66
```

```
DB 71 TAAGTACCTCGCGCGGACACGC 48

RESULT 75
US-10-357-930-45120/c
; Sequence 45120, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45120
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-45120

Query Match      1.4%; Score 24; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
DB 101 TAAGTACCTCGCGCGGACACGC 78

RESULT 76
US-10-001-857-66/c
; Sequence 66, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-857-66
```

```
Query Match      1.4%; Score 24; DB 5; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACACGC 1713
Db      24 TAAGTACCTCGCGCGGACACGC 1

RESULT 77
US-09-814-353-18705/c
; Sequence 18705, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18705
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-18705

Query Match      1.4%; Score 24; DB 3; Length 460;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACACGC 1713
Db      108 TAAGTACCTCGCGCGGACACGC 85

RESULT 78
US-10-198-846-5501/c
; Sequence 5501, Application US/10198846
; Publication No. US2003099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5501
; LENGTH: 463
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18, 43, 86, 88, 89, 264, 388, 407, 432
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-5501

Query Match      1.4%; Score 24; DB 5; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACACGC 1713
Db      116 TAAGTACCTCGCGCGGACACGC 93

RESULT 79
US-09-814-353-3344/c
; Sequence 3344, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3344
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 99, 279, 300, 303, 315, 331, 344, 352, 356, 371, 377, 380,
; LOCATION: 383, 393, 403, 417, 422, 428, 431
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-3344

Query Match      1.4%; Score 24; DB 3; Length 464;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACACGC 1713
Db      30 TAAGTACCTCGCGCGGACACGC 7

RESULT 80
US-09-814-353-9665/c
; Sequence 9665, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
```

```
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
/ FILE REFERENCE: MRI-006B
/ CURRENT APPLICATION NUMBER: US/09/814,353
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: US 60/191,031
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/207,124
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: US 60/211,940
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: US 60/216,820
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: US 60/220,661
/ PRIOR FILING DATE: 2000-07-25
/ PRIOR APPLICATION NUMBER: US 60/257,672
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 22037
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9665
/ LENGTH: 464
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 99, 279, 300, 303, 315, 331, 344, 352, 356, 371, 377, 380,
/ LOCATION: 383, 393, 403, 417, 422, 428, 431
/ OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9665

Query Match 1.4%; Score 24; DB 3; Length 464;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 30 TAAGTACCTCGGCGGACACGC 7

RESULT 81
US-09-814-353-15851/c
/ Sequence 15851, Application US/09814353
/ Publication No. US20030165831A1
/ GENERAL INFORMATION:
/ APPLICANT: Thompson, Pamela
/ APPLICANT: Lillie, James
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
/ FILE REFERENCE: MRI-006B
/ CURRENT APPLICATION NUMBER: US/09/814,353
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: US 60/191,031
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/207,124
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: US 60/211,940
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: US 60/216,820
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: US 60/220,661
/ PRIOR FILING DATE: 2000-07-25
/ PRIOR APPLICATION NUMBER: US 60/257,672
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 22037
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 15851
/ LENGTH: 471
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-814-353-15851
```

```
Query Match 1.4%; Score 24; DB 3; Length 471;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 103 TAAGTACCTCGGCGGACACGC 80

RESULT 82
US-09-814-353-4472/c
/ Sequence 4472, Application US/09814353
/ Publication No. US20030165831A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, John
/ APPLICANT: Thompson, Pamela
/ APPLICANT: Lillie, James
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
/ FILE REFERENCE: MRI-006B
/ CURRENT APPLICATION NUMBER: US/09/814,353
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: US 60/191,031
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/207,124
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: US 60/211,940
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: US 60/216,820
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: US 60/220,661
/ PRIOR FILING DATE: 2000-07-25
/ PRIOR APPLICATION NUMBER: US 60/257,672
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 22037
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4472
/ LENGTH: 486
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 31, 98, 159, 166, 289, 348, 361, 364, 385, 393, 398, 400,
/ LOCATION: 403, 410, 414, 419, 432, 457, 467
/ OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4472

Query Match 1.4%; Score 24; DB 3; Length 486;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGGACACGC 1713
Db 30 TAAGTACCTCGGCGGACACGC 7

RESULT 83
US-09-814-353-10775/c
/ Sequence 10775, Application US/09814353
/ Publication No. US20030165831A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, John
/ APPLICANT: Thompson, Pamela
/ APPLICANT: Lillie, James
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
/ FILE REFERENCE: MRI-006B
/ CURRENT APPLICATION NUMBER: US/09/814,353
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: US 60/191,031
```

```
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10775
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31, 98, 159, 166, 289, 348, 361, 364, 385, 393, 398, 400,
; LOCATION: 403, 410, 414, 419, 432, 457, 467
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-10775

Query Match 1.4%; Score 24; DB 3; Length 486;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 84
US-09-814-353-16367/c
; Sequence 16367, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16367
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 221
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-16367

Query Match 1.4%; Score 24; DB 3; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.13;
```

```
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 85 TAAGTACCTCGCGCGGACACGC 62

RESULT 85
US-09-814-353-15976/c
; Sequence 15976, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15976
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-15976

Query Match 1.4%; Score 24; DB 3; Length 517;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 102 TAAGTACCTCGCGCGGACACGC 79

RESULT 86
US-09-814-353-4993/c
; Sequence 4993, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
```



```
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4993
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 443, 491
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4993
```

```
Query Match 1.4%; Score 24; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACCTCGCGCGACACGC 7
```

RESULT 87

```
US-09-814-353-11286/c
; Sequence 11286, Application US/09814353
; Publication No. US20030165831A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
```

```
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11286
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 443, 491
; OTHER INFORMATION: n = A,T,C or G
```

US-09-814-353-11286

```
Query Match 1.4%; Score 24; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 30 TAAGTACCTCGCGCGACACGC 7
```

RESULT 88

```
US-09-814-353-15615/c
```

```
; Sequence 15615, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
```

```
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15615
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-09-814-353-15615

```
Query Match 1.4%; Score 24; DB 3; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1690 TAAGTACCTCGCGCGACACGC 1713
|||||
Db 106 TAAGTACCTCGCGCGACACGC 83
```

RESULT 89

```
US-09-814-353-17892/c
; Sequence 17892, Application US/09814353
; Publication No. US20030165831A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
```

```
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17892
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```

; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12105
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 435
; OTHER INFORMATION: n = A,T,C or G
; US-09-814-353-12105

Query Match 1.4%; Score 24; DB 3; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGGCGCGACCAACGC 1713
DB 30 TAAGTACCTCGGCGCGACCAACGC 7

RESULT 92
US-09-814-353-17394/c
; Sequence 17394, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17394
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 495
; OTHER INFORMATION: n = A,T,C or G
; US-09-814-353-17394

```

Query Match 1.4%; Score 24; DB 3; Length 546;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 105 TAAGTACCTCGCGCGGACACGC 82

RESULT 93

US-09-814-353-6042/c
; Sequence 6042, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6042
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 388, 442, 468, 478, 503, 540
; OTHER INFORMATION: n = A,T,C or G

US-09-814-353-6042
Query Match 1.4%; Score 24; DB 3; Length 548;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 94

US-09-814-353-12321/c
; Sequence 12321, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12321
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 388, 442, 468, 478, 503, 540
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-12321

Query Match 1.4%; Score 24; DB 3; Length 548;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
Db 30 TAAGTACCTCGCGCGGACACGC 7

RESULT 95

US-10-357-930-39396/c
; Sequence 39396, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39396
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-39396

Query Match 1.4%; Score 24; DB 8; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 TAAGTACCTCGCGCGGACACGC 1713
|||||

```
Db      85 TAAGTACCTCGCGCGGACCACGC 62

RESULT 96
US-10-357-930-43996/c
; Sequence 43996, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43996
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-43996

Query Match      1.4%; Score 24; DB 8; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACCACGC 1713
      |||
Db      85 TAAGTACCTCGCGCGGACCACGC 62

RESULT 97
US-09-814-353-18489/c
; Sequence 18489, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-005B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672

US-09-814-353-18489
; Sequence 18489, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43996
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-43996

Query Match      1.4%; Score 24; DB 8; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACCACGC 1713
      |||
Db      85 TAAGTACCTCGCGCGGACCACGC 62

RESULT 98
US-10-357-930-36049
; Sequence 36049, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36049
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-36049

Query Match      1.4%; Score 24; DB 8; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1690 TAAGTACCTCGCGCGGACCACGC 1713
      |||
Db      351 TAAGTACCTCGCGCGGACCACGC 374

RESULT 99
US-10-357-930-45110
; Sequence 45110, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
```

```

; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4510
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-45110

```

```

Query Match      1.4%; Score 24; DB 8; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGGACCCAGC 1713
Db 351 TAAGTACCTCGCGCGGACCCAGC 374

```

```

RESULT 100
US-10-950-009-112/c
; Sequence 112, Application US/10950009
; Publication No. US2005006934A1
; GENERAL INFORMATION:
; APPLICANT: BERKA, Randy
; APPLICANT: BASHKIROVA, Elena
; APPLICANT: REV, Michael
; TITLE OF INVENTION: Methods For Monitoring Gene Expression
; FILE REFERENCE: 10541.200-US
; CURRENT APPLICATION NUMBER: US/10/950,009
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: 60/506,140
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 1190
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Trichoderma reesei
US-10-950-009-112

```

```

Query Match      1.4%; Score 24; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1690 TAAGTACCTCGCGCGGACCCAGC 1713
Db 24 TAAGTACCTCGCGCGGACCCAGC 1

```

Search completed: March 11, 2006, 22:31:51
Job time : 1455 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 21:01:03 ; Search time 679 Seconds
(without alignments)
5820.912 Million cell updates/sec

Title: US-09-989-890-105

Perfect score: 1713

Sequence: 1 agccccgcctggacaccc.....tacctcgccggaccacgc 1713

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 7673375 seqs, 1153648444 residues

Word size : 0

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published Applications NA_New.*

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1594	93.1	1785	9	US-11-072-512-799
c	25	1.5	25	8	US-10-310-914A-1045304
c	3	25	1.5	8	US-10-310-914A-1045320
c	4	25	1.5	12	US-11-121-849-344330
5	25	1.5	25	12	US-11-121-849-344331
6	25	1.5	25	12	US-11-121-849-344332
7	25	1.5	25	12	US-11-121-849-344333
8	25	1.5	25	12	US-11-121-849-344334
9	25	1.5	25	12	US-11-121-849-344335
10	25	1.5	25	12	US-11-121-849-344336
11	25	1.5	25	12	US-11-121-849-344337
12	25	1.5	25	12	US-11-121-849-344338
13	25	1.5	25	12	US-11-121-849-344339
14	25	1.5	25	12	US-11-121-849-344340
15	25	1.5	25	12	US-11-121-849-344517
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17	25	1.5	25	12	US-11-121-849-344519
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22	25	1.5	25	12	US-11-121-849-344524	Sequence 344524,
23	25	1.5	25	12	US-11-121-849-344525	Sequence 344525,
24	25	1.5	25	12	US-11-121-849-344526	Sequence 344526,
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c	34	1.5	25	12	US-10-310-914A-1045306	Sequence 1045306,
c	35	1.5	25	12	US-10-310-914A-1045307	Sequence 1045307,
c	36	1.5	25	12	US-10-310-914A-1045309	Sequence 1045309,
c	37	1.5	25	12	US-10-310-914A-1045310	Sequence 1045310,
c	38	1.5	25	12	US-10-310-914A-1045313	Sequence 1045313,
c	39	1.5	25	12	US-10-310-914A-1045314	Sequence 1045314,
c	40	1.5	25	12	US-10-310-914A-1045315	Sequence 1045315,
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c	44	1.5	25	12	US-10-310-914A-1045329	Sequence 1045329,
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c	47	1.5	25	12	US-10-310-914A-1045305	Sequence 1045305,
c	48	1.5	25	12	US-10-310-914A-1045333	Sequence 1045333,
c	49	1.5	25	12	US-11-234-786-293	Sequence 293, App
c	50	1.5	25	12	US-11-116-881A-2005	Sequence 2005, App
c	51	1.5	25	12	US-11-116-881A-992	Sequence 992, App
c	52	1.5	25	12	US-11-057-484A-13	Sequence 13, Appl
c	53	1.5	25	12	US-11-201-194-5	Sequence 5, Appl
c	54	1.5	25	12	US-11-206-587-4	Sequence 4, Appl
c	55	1.5	25	12	US-10-310-914A-1045308	Sequence 1045308,
c	56	1.5	25	12	US-10-310-914A-1045312	Sequence 1045312,
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c	60	1.5	25	12	US-11-136-527-193854	Sequence 193854,
c	61	1.5	25	12	US-11-031-356-14	Sequence 14, Appl
c	62	1.5	25	12	US-09-925-065A-613855	Sequence 613855,
c	63	1.5	25	12	US-11-136-527-3780	Sequence 3780, App
c	64	1.5	25	12	US-11-136-527-7876	Sequence 7876, App
c	65	1.5	25	12	US-10-750-185-36767	Sequence 36767, A
c	66	1.5	25	12	US-10-750-623-36767	Sequence 36767, A
c	67	1.5	25	12	US-11-096-568A-25683	Sequence 25683, A
c	68	1.5	25	12	US-11-136-527-3889	Sequence 3889, App
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149	19	1.1	19	11	US-11-083-784-1430759	Sequence 1430759,	222	19	1.1	300	12	US-11-234-786-297	Sequence 297, App
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153	19	1.1	19	11	US-11-083-784-1430763	Sequence 1430763,	226	19	1.1	371	8	US-10-623-155-139	Sequence 139, App
154	19	1.1	19	11	US-11-083-784-1430764	Sequence 1430764,	227	19	1.1	371	8	US-10-623-155-141	Sequence 141, App
155	19	1.1	19	11	US-11-083-784-1430765	Sequence 1430765,	228	19	1.1	371	8	US-10-623-155-145	Sequence 145, App
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157	19	1.1	19	11	US-11-083-784-1430767	Sequence 1430767,	230	19	1.1	431	12	US-11-108-172-622	Sequence 622, App
158	19	1.1	19	11	US-11-083-784-1430768	Sequence 1430768,	231	19	1.1	537	6	US-09-925-065A-814229	Sequence 814229,
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166	19	1.1	19	11	US-11-083-784-1430776	Sequence 1430776,	239	19	1.1	623	6	US-09-925-065A-910579	Sequence 910579,

C 240	19	1.1	639	6	US-09-925-065A-517828	Sequence 517828,	C 313	18	1.1	86764	7	US-10-330-773-600	Sequence 600, App
C 241	19	1.1	936	8	US-10-750-185-36256	Sequence 36256, A	C 314	18	1.1	114801	12	US-11-121-086-22	Sequence 22, Appl
C 242	19	1.1	936	8	US-10-750-623-36256	Sequence 36256, A	C 315	18	1.1	162537	12	US-11-121-086-59	Sequence 59, Appl
C 243	19	1.1	1524	8	US-10-750-185-58349	Sequence 58349, A	C 316	18	1.1	163162	12	US-11-121-086-66	Sequence 66, Appl
C 244	19	1.1	1524	8	US-10-750-623-58349	Sequence 58349, A	C 317	18	1.1	171732	12	US-11-121-086-98	Sequence 98, Appl
C 245	19	1.1	1734	12	US-11-112-908-363	Sequence 363, App	C 318	17	1.0	19	19	US-11-101-244-463615	Sequence 463615,
C 246	19	1.1	2799	6	US-09-925-065A-554137	Sequence 554137, A	C 319	17	1.0	19	11	US-11-083-784-463615	Sequence 815013,
C 247	19	1.1	3085	8	US-10-750-185-63119	Sequence 63119, A	C 320	17	1.0	20	8	US-10-310-914A-815013	Sequence 54638, A
C 248	19	1.1	3065	8	US-10-750-623-63119	Sequence 63119, A	C 321	17	1.0	25	7	US-10-932-182A-54638	Sequence 54638, A
C 249	19	1.1	4364	9	US-11-245-147-172	Sequence 172, App	C 322	17	1.0	25	7	US-10-932-182A-54638	Sequence 7454, Ap
C 250	19	1.1	4364	9	US-11-245-147-233	Sequence 233, App	C 323	17	1.0	25	12	US-11-121-849-7454	Sequence 398779,
C 251	19	1.1	6087	12	US-11-000-463-485	Sequence 485, App	C 324	17	1.0	25	12	US-11-121-849-7454	Sequence 398779,
C 252	19	1.1	18930	8	US-10-995-561-13213	Sequence 13213, A	C 325	17	1.0	25	12	US-11-121-849-400152	Sequence 400152,
C 253	19	1.1	16194	12	US-11-112-908-57	Sequence 57, Appl	C 326	17	1.0	25	12	US-11-136-527-193853	Sequence 193825,
C 254	18	1.1	18	8	US-10-310-914A-1045316	Sequence 1045316,	C 327	17	1.0	25	12	US-11-136-527-193853	Sequence 193853,
C 255	18	1.1	18	8	US-10-310-914A-1045317	Sequence 1045317,	C 328	17	1.0	40	7	US-10-989-767A-664	Sequence 26, Appl
C 256	18	1.1	18	8	US-10-310-914A-1045326	Sequence 1045326,	C 329	17	1.0	40	7	US-10-989-767A-664	Sequence 664, App
C 257	18	1.1	18	8	US-10-310-914A-1045336	Sequence 1045336,	C 330	17	1.0	40	7	US-10-989-767A-664	Sequence 755, App
C 258	18	1.1	20	7	US-10-753-195-30	Sequence 30, Appl	C 331	17	1.0	40	12	US-10-859-643-755	Sequence 755, App
C 259	18	1.1	20	7	US-10-989-767A-668	Sequence 668, App	C 332	17	1.0	40	12	US-11-097-864-755	Sequence 755, App
C 260	18	1.1	20	12	US-11-097-864-759	Sequence 759, App	C 333	17	1.0	201	8	US-10-995-561-26993	Sequence 26993, A
C 261	18	1.1	20	12	US-11-097-864-759	Sequence 759, App	C 334	17	1.0	201	8	US-10-995-561-26993	Sequence 26993, A
C 262	18	1.1	20	12	US-11-097-912-759	Sequence 759, App	C 335	17	1.0	201	8	US-10-995-561-32420	Sequence 32420, A
C 263	18	1.1	25	12	US-11-136-527-193846	Sequence 193846,	C 336	17	1.0	201	8	US-10-995-561-32430	Sequence 32430, A
C 264	18	1.1	25	12	US-11-136-527-193867	Sequence 193867,	C 337	17	1.0	231	7	US-10-932-182A-3666	Sequence 3666, Ap
C 265	18	1.1	65	8	US-10-310-914A-12176	Sequence 12176, A	C 338	17	1.0	231	7	US-10-932-182A-3666	Sequence 3666, Ap
C 266	18	1.1	201	8	US-10-995-561-61967	Sequence 61967, A	C 339	17	1.0	368	12	US-11-000-688-229	Sequence 229, App
C 267	18	1.1	201	8	US-10-995-561-62068	Sequence 62068, A	C 340	17	1.0	387	7	US-10-932-182A-79065	Sequence 79065, A
C 268	18	1.1	201	12	US-11-124-368A-3102	Sequence 3102, Ap	C 341	17	1.0	387	7	US-10-932-182A-79065	Sequence 79065, A
C 269	18	1.1	201	12	US-11-124-368A-4125	Sequence 4125, Ap	C 342	17	1.0	387	7	US-10-932-182A-79065	Sequence 79065, A
C 270	18	1.1	301	12	US-11-000-688-91	Sequence 91, Appl	C 343	17	1.0	407	6	US-09-925-065A-507912	Sequence 507912,
C 271	18	1.1	301	12	US-11-234-778-230	Sequence 230, App	C 344	17	1.0	407	6	US-09-925-065A-507912	Sequence 507912,
C 272	18	1.1	512	6	US-09-925-065A-8330825	Sequence 8330825,	C 345	17	1.0	437	6	US-09-925-065A-216304	Sequence 216304,
C 273	18	1.1	512	6	US-09-925-065A-8330825	Sequence 8330825,	C 346	17	1.0	444	12	US-11-000-688-1577	Sequence 1577, Ap
C 274	18	1.1	563	6	US-09-925-065A-353713	Sequence 353713,	C 347	17	1.0	458	6	US-09-925-065A-401869	Sequence 401869,
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C 277	18	1.1	570	6	US-09-925-065A-738650	Sequence 738650,	C 350	17	1.0	472	12	US-11-108-172-94	Sequence 94, Appl
C 278	18	1.1	570	6	US-09-925-065A-738651	Sequence 738651,	C 351	17	1.0	479	6	US-09-925-065A-318342	Sequence 318342,
C 279	18	1.1	582	6	US-09-925-065A-134986	Sequence 134986,	C 352	17	1.0	502	6	US-09-925-065A-398434	Sequence 398434,
C 280	18	1.1	607	6	US-09-925-065A-513479	Sequence 513479,	C 353	17	1.0	503	6	US-09-925-065A-379105	Sequence 379105,
C 281	18	1.1	614	6	US-09-925-065A-374068	Sequence 374068,	C 354	17	1.0	504	6	US-09-925-065A-334102	Sequence 334102,
C 282	18	1.1	614	6	US-09-925-065A-646302	Sequence 646302,	C 355	17	1.0	508	6	US-09-925-065A-149410	Sequence 149410,
C 283	18	1.1	615	6	US-09-925-065A-375993	Sequence 375993,	C 356	17	1.0	512	12	US-11-108-172-88	Sequence 88, Appl
C 284	18	1.1	615	6	US-09-925-065A-375994	Sequence 375994,	C 357	17	1.0	517	6	US-09-925-065A-510849	Sequence 510849,
C 285	18	1.1	619	6	US-09-925-065A-385595	Sequence 385595,	C 358	17	1.0	520	6	US-09-925-065A-457399	Sequence 457399,
C 286	18	1.1	619	6	US-09-925-065A-385596	Sequence 385596,	C 359	17	1.0	529	6	US-09-925-065A-378664	Sequence 378664,
C 287	18	1.1	619	6	US-09-925-065A-385597	Sequence 385597,	C 360	17	1.0	529	6	US-09-925-065A-536447	Sequence 536447,
C 288	18	1.1	626	6	US-09-925-065A-259994	Sequence 259994,	C 361	17	1.0	529	6	US-09-925-065A-536448	Sequence 536448,
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C 291	18	1.1	638	6	US-09-925-065A-826845	Sequence 826845,	C 364	17	1.0	538	6	US-09-925-065A-9956	Sequence 9956, Ap
C 292	18	1.1	638	6	US-09-925-065A-834468	Sequence 834468,	C 365	17	1.0	545	6	US-09-925-065A-624168	Sequence 624168,
C 293	18	1.1	639	6	US-09-925-065A-482417	Sequence 482417,	C 366	17	1.0	548	6	US-09-925-065A-52567	Sequence 52567, A
C 294	18	1.1	640	6	US-09-925-065A-826248	Sequence 826248,	C 367	17	1.0	548	6	US-09-925-065A-52567	Sequence 52567, A
C 295	18	1.1	656	6	US-09-925-065A-716809	Sequence 716809,	C 368	17	1.0	548	6	US-09-925-065A-181548	Sequence 181548,
C 296	18	1.1	661	6	US-09-925-065A-917118	Sequence 917118,	C 369	17	1.0	549	6	US-09-925-065A-476079	Sequence 476079,
C 297	18	1.1	777	7	US-10-932-182A-4384	Sequence 4384, Ap	C 370	17	1.0	549	6	US-09-925-065A-476080	Sequence 476080,
C 298	18	1.1	777	7	US-10-932-182A-4384	Sequence 4384, Ap	C 371	17	1.0	549	6	US-09-925-065A-476081	Sequence 476081,
C 299	18	1.1	845	12	US-11-150-888-22	Sequence 22, Appl	C 372	17	1.0	549	6	US-09-925-065A-476082	Sequence 476082,
C 300	18	1.1	1094	6	US-09-925-065A-720390	Sequence 720390,	C 373	17	1.0	549	6	US-09-925-065A-861215	Sequence 861215,
C 301	18	1.1	1303	8	US-10-750-185-42410	Sequence 42410, A	C 374	17	1.0	550	6	US-09-925-065A-934849	Sequence 934849,
C 302	18	1.1	1303	8	US-10-750-623-42410	Sequence 42410, A	C 375	17	1.0	551	6	US-09-925-065A-512767	Sequence 512767,
C 303	18	1.1	1548	8	US-10-775-169-178	Sequence 178, App	C 376	17	1.0	553	6	US-09-925-065A-389617	Sequence 389617,
C 304	18	1.1	1563	8	US-10-750-185-26090	Sequence 26090, A	C 377	17	1.0	553	6	US-09-925-065A-389618	Sequence 389618,
C 305	18	1.1	1563	8	US-10-750-623-26090	Sequence 26090, A	C 378	17	1.0	555	6	US-09-925-065A-90074	Sequence 90074, A
C 306	18	1.1	1814	8	US-10-750-185-51351	Sequence 51351, A	C 379	17	1.0	559	6	US-09-925-065A-480681	Sequence 480681,
C 307	18	1.1	1814	8	US-10-750-623-51351	Sequence 51351, A	C 380	17	1.0	559	6	US-09-925-065A-480682	Sequence 480682,
C 308	18	1.1	2454	9	US-11-072-512-275	Sequence 275, App	C 381	17	1.0	560	6	US-09-925-065A-942690	Sequence 942690,
C 309	18	1.1	2625	9	US-11-072-512-296	Sequence 296, App	C 382	17	1.0	562	6	US-09-925-065A-237859	Sequence 237859,
C 310	18	1.1	2845	6	US-09-925-065A-681694	Sequence 681694,	C 383	17	1.0	564	6	US-09-925-065A-451113	Sequence 451113,
C 311	18	1.1	3496	9	US-11-072-512-1039	Sequence 1039, Ap	C 384	17	1.0	574	6	US-09-925-065A-511080	Sequence 511080,
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C 387	17	1.0	578	6	US-09-925-065A-353773	Sequence 353773,	17	1.0	690	6	US-09-925-065A-549864	Sequence 549864,
C 388	17	1.0	581	6	US-09-925-065A-467016	Sequence 467016,	17	1.0	695	8	US-10-750-185-62194	Sequence 62194, A
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C 391	17	1.0	582	6	US-09-925-065A-93183	Sequence 93183, A	17	1.0	705	6	US-09-925-065A-920031	Sequence 920031,
C 392	17	1.0	583	6	US-09-925-065A-275934	Sequence 275934,	17	1.0	710	12	US-11-136-527-1607	Sequence 1607, Ap
C 393	17	1.0	587	6	US-09-925-065A-773249	Sequence 773249,	17	1.0	717	6	US-09-925-065A-920100	Sequence 920100,
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C 400	17	1.0	591	6	US-09-925-065A-93648	Sequence 93648, A	17	1.0	801	8	US-10-750-185-56880	Sequence 56880, A
C 401	17	1.0	594	6	US-09-925-065A-400035	Sequence 400035,	17	1.0	801	8	US-10-750-623-56880	Sequence 56880, A
C 402	17	1.0	598	6	US-09-925-065A-303099	Sequence 303099,	17	1.0	838	6	US-09-925-065A-919345	Sequence 919345,
C 403	17	1.0	600	8	US-10-750-185-20043	Sequence 20043, A	17	1.0	841	6	US-09-925-065A-924260	Sequence 924260,
C 404	17	1.0	600	8	US-10-750-623-20043	Sequence 20043, A	17	1.0	841	6	US-09-925-065A-924261	Sequence 924261,
C 405	17	1.0	600	12	US-11-136-527-4791	Sequence 4791, Ap	17	1.0	879	12	US-11-055-822-133	Sequence 133, App
C 406	17	1.0	600	12	US-11-136-527-5703	Sequence 5703, Ap	17	1.0	879	12	US-11-055-822-1119	Sequence 1119, Ap
C 407	17	1.0	605	6	US-09-925-065A-73280	Sequence 73280, A	17	1.0	917	6	US-09-925-065A-690458	Sequence 690458,
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C 424	17	1.0	628	6	US-09-925-065A-632812	Sequence 632812,	17	1.0	1360	8	US-10-750-623-26652	Sequence 26652, A
C 425	17	1.0	628	6	US-09-925-065A-632813	Sequence 632813,	17	1.0	1378	9	US-11-096-568A-5536	Sequence 5536, Ap
C 426	17	1.0	630	6	US-09-925-065A-509224	Sequence 509224,	17	1.0	1316	9	US-11-096-568A-5536	Sequence 5536, Ap
C 427	17	1.0	631	6	US-09-925-065A-54555	Sequence 54555,	17	1.0	1316	9	US-11-096-568A-5536	Sequence 5536, Ap
C 428	17	1.0	631	6	US-09-925-065A-54556	Sequence 54556, A	17	1.0	1337	8	US-10-750-185-25170	Sequence 25170, A
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ALIGNMENTS

RESULT 1

US-11-072-512-799
; Sequence 799, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAL, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
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; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
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NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 799
LENGTH: 1785
TYPE: DNA
ORGANISM: Homo sapiens
US-11-072-512-799

Query Match 93.1%; Score 1594; DB 9; Length 1785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCCCGCCCTGACACCCGCCCGCAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG 60
DB 90 ATGCCCGCCCTGACACCCGCCCGCAGCATCTGGGCTCCACGCTTGGGACCGTGGGAG 149

QY 61 CGGCCAACAGAGTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACAACGCCG 120
DB 150 CGGCCAACAGAGTATGTCTGGAGACATATGATAAACACCTCAGCCCCCACAACGCCG 209

QY 121 CGCACCCGTAGACAGACCCCAAGGACCTGGCCACATGAGGCGCAGAGCATTTACCTTC 180
DB 210 CGCACCCGTAGACAGACCCCAAGGACCTGGCCACATGAGGCGCAGAGCATTTACCTTC 269

QY 181 ATCTCTGGCTCTGCTGAGCGCGCCCTTGTAGTCCGCCACCTGCTGCTCTGGCGACCC 240
DB 270 ATCTCTGGCTCTGCTGAGCGCGCCCTTGTAGTCCGCCACCTGCTGCTCTGGCGACCC 329

QY 241 TGGGCTGGAGGTGTGCGCGGCTGCTCTTGTCTCCGCGCTGCGGGAATGCTCTCCAG 300
DB 330 TGGGCTGGAGGTGTGCGCGGCTGCTCTTGTCTCCGCGCTGCGGGAATGCTCTCCAG 389

QY 301 CGGTGTGGAGCTGTGTGGGGATGCGAGCCCTGCTGTCTACTGAGGACTCCACTGAG 360
DB 390 CGGTGTGGAGCTGTGTGGGGATGCGAGCCCTGCTGTCTACTGAGGACTCCACTGAG 449

QY 361 GGGACTGCTGAAGCAACTGGGCCAAGGAGCAATGAGGTGCCCGCCAGCCCTGATCT 420
DB 450 GGGACTGCTGAAGCAACTGGGCCAAGGAGCAATGAGGTGCCCGCCAGCCCTGATCT 509

QY 421 GCACCCCGCAGCGCGGATGCGCCAGCGCTCAAGTCAACCATGGGCGAGCAGCTTCAGC 480
DB 510 GCACCCCGCAGCGCGGATGCGCCAGCGCTCAAGTCAACCATGGGCGAGCAGCTTCAGC 569

QY 481 TACCCCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTTACCCGAGGCGCACTCCCA 540
DB 570 TACCCCGATGTTAAGCTCAAGGATCCCTGTGTATCCCTTACCCGAGGCGCACTCCCA 629

QY 541 GCGCTGTAGCGGACTCTGCTGCAAGGAGCCACTGCGCGATCCCGCCACCATGGACAC 600
DB 630 GCGCTGTAGCGGACTCTGCTGCAAGGAGCCACTGCGCGATCCCGCCACCATGGACAC 689

QY 601 AGCCTGCCAGCACCTTTGCGAGTAGTCTCTGGGCTCCGAGGAGTACTATTCTTTCCAT 660
DB 690 AGCCTGCCAGCACCTTTGCGAGTAGTCTCTGGGCTCCGAGGAGTACTATTCTTTCCAT 749

QY 661 GAGTCGGAAGCTGAGCTGCGGAGATGGGAGTGGCTTCCATGTGAGCGCGAGAAATGTAT 720
DB 750 GAGTCGGAAGCTGAGCTGCGGAGATGGGAGTGGCTTCCATGTGAGCGCGAGAAATGTAT 809

QY 721 GTGCTCATCTTCAAGAGCTGACAGAGCTTTGAGGCTACACAGATCGATGAGCTGGCC 780
DB 810 GTGCTCATCTTCAAGAGCTGACAGAGCTTTGAGGCTACACAGATCGATGAGCTGGCC 869

QY 781 AAGTGACATCAGACACTGTGTTCTCGGAGAGACAGTAAAGATCTCGGACCTTATCAGC 840
DB 870 AAGTGACATCAGACACTGTGTTCTCGGAGAGACAGTAAAGATCTCGGACCTTATCAGC 929

RESULT 2

US-10-310-914A-1045304/c
; Sequence 1045304, Application US/10310914A
; Publication No. US2006000332A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06

QY 841 AGCATCAGCAGGACTACCACTGGATGACAGGATGCTTGAGGGCGCCTGGTACGGGC 900
DB 930 AGCATCAGCAGGACTACCACTGGATGACAGGATGCTTGAGGGCGCCTGGTACGGGC 989

QY 901 ATCAATTCGCATTTAGTACCCGAAAGAGCCGCTGCTCGCCCAAGACCTCGGAGGGTCTGTTCA 960
DB 990 ATCAATTCGCATTTAGTACCCGAAAGAGCCGCTGCTCGCCCAAGACCTCGGAGGGTCTGTTCA 1049

QY 961 ACTCGGGCTGCTGCCCAACCGCTGCTGCCCTTGAAGTGGCCATGAGACCATGTTGGGC 1020
DB 1050 ACTCGGGCTGCTGCCCAACCGCTGCTGCCCTTGAAGTGGCCATGAGACCATGTTGGGC 1109

QY 1021 TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGATGAGATGCC 1080
DB 1110 TCAGGTCTCAGCCAGGATGAGCTGACAGTGCAGATCTCCAGGAGACGATGAGATGCC 1169

QY 1081 ATGCCCGGAAAGCTGAGGCTTATGAGGCTTCAGGCTACCCAGCAAGACCATGATCATCC 1140
DB 1170 ATGCCCGGAAAGCTGAGGCTTATGAGGCTTCAGGCTACCCAGCAAGACCATGATCATCC 1229

QY 1141 TTCAGGGGCAACGACACAGACTGCTCGGGGGCAACCTTGTCTCAGGTGTACTGTCAACC 1200
DB 1230 TTCAGGGGCAACGACACAGACTGCTCGGGGGCAACCTTGTCTCAGGTGTACTGTCAACC 1289

QY 1201 CTGCCAGGCGCAGCTGCCACACCCCTTCTGGGAGAGCATGGCCTACAGAAATGAAGGG 1260
DB 1290 CTGCCAGGCGCAGCTGCCACACCCCTTCTGGGAGAGCATGGCCTACAGAAATGAAGGG 1349

QY 1261 GGACCAAGGAACCCCTGTCGGGAGAGGCTTAGACCTGAAAGCAGTGCACCATCTGGCTCTCC 1320
DB 1350 GGACCAAGGAACCCCTGTCGGGAGAGGCTTAGACCTGAAAGCAGTGCACCATCTGGCTCTCC 1409

QY 1321 TGCCTTGGCTGACTGGGTTCTGGACCATGTGCAATTTCACTGGGCGCATGGGATCTAATC 1380
DB 1410 TGCCTTGGCTGACTGGGTTCTGGACCATGTGCAATTTCACTGGGCGCATGGGATCTAATC 1469

QY 1381 TCTCTGCATCCCGAGCTGCTGATCCCTGCGAGGCGCCTTCTTCTGCTCATGGTCT 1440
DB 1470 TCTCTGCATCCCGAGCTGCTGATCCCTGCGAGGCGCCTTCTTCTGCTCATGGTCT 1529

QY 1441 TCAGGTGGGCTCATCATGGAAGTAAAGGAGTTAGGATTAACCTTCTGGGAGTGAACCTG 1500
DB 1530 TCAGGTGGGCTCATCATGGAAGTAAAGGAGTTAGGATTAACCTTCTGGGAGTGAACCTG 1589

QY 1501 ACTCCATCCCCCTATTGCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAAT 1560
DB 1590 ACTCCATCCCCCTATTGCCACCCCTAACCAATCATGCAAACTTCTCCCTCCCTGGGGTAAAT 1649

QY 1561 TCACAGTTTAAAGAGCTTATCTTAATGTATTGTATTGGGGGGTGGGCGAGGGCCCACT 1620
DB 1650 TCACAGTTTAAAGAGCTTATCTTAATGTATTGTATTGGGGGGTGGGCGAGGGCCCACT 1709

QY 1621 CTATGTATTGTTAAAGAGTTGTTCTGCTGTTCTGGCTGATGTTCTGTATCTTAACATGAC 1680
DB 1710 CTATGTATTGTTAAAGAGTTGTTCTGCTGTTCTGGCTGATGTTCTGTATCTTAACATGAC 1769

QY 1681 CACAGTTTCTAAGTAC 1696
DB 1770 CACAGTTTCTAAGTAC 1785

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045304
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045304

Query Match 1.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1475 GCATTACCTTCGGGAGTGAACCT 1499
|||||
Db 25 GCATTACCTTCGGGAGTGAACCT 1

RESULT 3

US-10-310-914A-1045320/c
; Sequence 1045320 Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045320
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045320

Query Match 1.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1382 CCTTGATCCCCAGCTGGTCTGATC 1406
|||||
Db 25 CCTTGATCCCCAGCTGGTCTGATC 1

RESULT 4

US-11-121-849-344330
; Sequence 344330, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344330
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344330

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1341 CTGGACCATGTGCATTTCACTGGC 1365
|||||

Db 1 CTGGACCATGTGCATTTCACTGGC 25

RESULT 5

US-11-121-849-344331
; Sequence 344331, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344331
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344331

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1356 TTCACTGGGCCATGGGATCTACATC 1380
|||||
Db 1 TTCACTGGGCCATGGGATCTACATC 25

RESULT 6

US-11-121-849-344332
; Sequence 344332, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344332
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344332

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1233 AGAAGCATGGCCTCAGAAATGAAGA 1257
|||||
Db 1 AGAAGCATGGCCTCAGAAATGAAGA 25

RESULT 7

US-11-121-849-344333
; Sequence 344333, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344333
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344336

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 CTGGCCATGGGATCTACATCTCTCT 1384
|||||
Db 1 CTGGCCATGGGATCTACATCTCTCT 25

RESULT 8

US-11-121-849-344334
; Sequence 344334, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344334
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344334

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 TGCTCATGCTTCAGGTGGCCTGA 1453
|||||
Db 1 TGCTCATGCTTCAGGTGGCCTGA 25

RESULT 9

US-11-121-849-344335
; Sequence 344335, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344335

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1466 AGGAGTTAGGCATTACCTTCTGGGA 1490
|||||
Db 1 AGGAGTTAGGCATTACCTTCTGGGA 25

RESULT 10

US-11-121-849-344336
; Sequence 344336, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344336
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344336

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 TACCTTCTGGGAGTGAACCTTGACT 1503
|||||
Db 1 TACCTTCTGGGAGTGAACCTTGACT 25

RESULT 11

US-11-121-849-344337
; Sequence 344337, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344337
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344337

Query Match 1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 ACCTTCTGGGAGTGAACCTTGACTC 1504
|||||
Db 1 ACCTTCTGGGAGTGAACCTTGACTC 25

RESULT 12

US-11-121-849-344338
; Sequence 344338, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma

```
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344338
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344338

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 GAACCCCTGTGGGAGAGGCTTAGAC 1292
      |||||
Db 1 GAACCCCTGTGGGAGAGGCTTAGAC 25

RESULT 13
US-11-121-849-344339
; Sequence 344339, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344339
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344339

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1273 CCTGTGGGAGAGGCTTAGACCTGAA 1297
      |||||
Db 1 CCTGTGGGAGAGGCTTAGACCTGAA 25

RESULT 14
US-11-121-849-344340
; Sequence 344340, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344340
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
```

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US-11-121-849-344340

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1318 TCCTGCTTGGCTGACTGGGTTCCT 1342
      |||||
Db 1 TCCTGCTTGGCTGACTGGGTTCCT 25

RESULT 15
US-11-121-849-344517
; Sequence 344517, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344517
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344517

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1356 TTCACCTGGGCCATGGGATCTACATC 1380
      |||||
Db 1 TTCACCTGGGCCATGGGATCTACATC 25

RESULT 16
US-11-121-849-344518
; Sequence 344518, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344518
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344518

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1357 TCACTGGGCCATGGGATCTACATCT 1381
      |||||
Db 1 TCACTGGGCCATGGGATCTACATCT 25

RESULT 17
US-11-121-849-344519
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```
; Sequence 344519, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344519
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344519

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1359 ACTGGCCATGGGATCTACATCTCC 1383
Db 1 ACTGGCCATGGGATCTACATCTCC 25

RESULT 18
US-11-121-849-344520
; Sequence 344520, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344520

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1359 ACTGGCCATGGGATCTACATCTCC 1383
Db 1 ACTGGCCATGGGATCTACATCTCC 25

RESULT 19
US-11-121-849-344521
; Sequence 344521, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344521
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344521

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 CTGGCCATGGGATCTACATCTCT 1384
Db 1 CTGGCCATGGGATCTACATCTCT 25
```

```
; SEQ ID NO 344521
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344521

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1464 TAAGGAGTTAGGCATTACCTTCTGG 1488
Db 1 TAAGGAGTTAGGCATTACCTTCTGG 25

RESULT 20
US-11-121-849-344522
; Sequence 344522, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344522
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344522

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1466 AGGAGTTAGGCATTACCTTCTGGGA 1490
Db 1 AGGAGTTAGGCATTACCTTCTGGGA 25

RESULT 21
US-11-121-849-344523
; Sequence 344523, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 60/567,949
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344523
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344523

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1467 GGAGTTAGGCATTACCTTCTGGGAG 1491
Db 1 GGAGTTAGGCATTACCTTCTGGGAG 25
```

```
RESULT 22
US-11-121-849-344524
; Sequence 344524, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344524
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344524

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 TACCTTCTGGGAGTGAACCTGACT 1503
      ||||||||||||||||||||||||
Db 1 TACCTTCTGGGAGTGAACCTGACT 25

RESULT 23
US-11-121-849-344525
; Sequence 344525, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344525
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344525

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 ACCTTCTGGGAGTGAACCTGACTC 1504
      ||||||||||||||||||||||||
Db 1 ACCTTCTGGGAGTGAACCTGACTC 25

RESULT 24
US-11-121-849-344526
; Sequence 344526, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
```

```
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344526

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 GAACCCCTGTGGAGAGGCTTAGAC 1292
      ||||||||||||||||||||||||
Db 1 GAACCCCTGTGGAGAGGCTTAGAC 25

RESULT 25
US-11-121-849-344527
; Sequence 344527, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 344527
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-344527

Query Match      1.5%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1273 CCTGTGGGAGAGGCTTAGACCTGAA 1297
      ||||||||||||||||||||||||
Db 1 CCTGTGGGAGAGGCTTAGACCTGAA 25

RESULT 26
US-10-310-914A-1045318/c
; Sequence 1045318, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045318
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045318

Query Match      1.4%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1378 ATCTCCTTCATCCCGAGCTGGTC 1401
Db 24 ATCTCCTTCATCCCGAGCTGGTC 1

RESULT 27
US-10-310-914A-1045328/c
; Sequence 1045328, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045328
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045328

Query Match 1.4%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1600 GGGGGGTGGCAGGCCCACTCTA 1623
Db 24 GGGGGGTGGCAGGCCCACTCTA 1

RESULT 28
US-10-310-914A-1045311/c
; Sequence 1045311, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045311
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045311

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1436 GGTCTTCAGGTGGCCTGATCATG 1458
Db 23 GGTCTTCAGGTGGCCTGATCATG 1

RESULT 29
US-10-310-914A-1045322/c
; Sequence 1045322, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045322
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045322

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1267 GGAACCCCTGTGGAGAGGCTTA 1289
Db 23 GGAACCCCTGTGGAGAGGCTTA 1

RESULT 30
US-10-310-914A-1045327/c
; Sequence 1045327, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045327
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045327

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1275 TGTGGGAGAGGCTTAGACCTGAA 1297

; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045322
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045322

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1593 TTGTATTGGGGTGGCAGGGC 1615
Db 23 TTGTATTGGGGTGGCAGGGC 1

RESULT 31
US-10-310-914A-1045337/c
; Sequence 1045337, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045337
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045337

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1267 GGAACCCCTGTGGAGAGGCTTA 1289
Db 23 GGAACCCCTGTGGAGAGGCTTA 1

RESULT 32
US-10-310-914A-1045337/c
; Sequence 1045337, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045337
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045337

Query Match 1.3%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1275 TGTGGGAGAGGCTTAGACCTGAA 1297


```
Db      23  TTGGGAGAGGCTTAGACCTGA 1
|||||
RESULT 32
US-10-310-914A-1045303/c
; Sequence 1045303, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045303
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045303

Query Match      1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1411 CCAGGGCCCTTCTCTCTGCT 1432
|||||
Db      22  CCAGGGCCCTTCTCTCTGCT 1

RESULT 33
US-10-310-914A-1045306/c
; Sequence 1045306, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045306
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045306

Query Match      1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1639 TTGGTCTGTTCTTGCTGAT 1660
|||||
Db      22  TTGGTCTGTTCTTGCTGAT 1

RESULT 34
US-10-310-914A-1045307/c
; Sequence 1045307, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
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; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045307
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045307

Query Match      1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1291 ACCTGAAGCAGTCCCACTCTG 1312
|||||
Db      22  ACCTGAAGCAGTCCCACTCTG 1

RESULT 35
US-10-310-914A-1045309/c
; Sequence 1045309, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045309
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045309

Query Match      1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1431 CTCATGCTCTCAGGTGGCTG 1452
|||||
Db      22  CTCATGCTCTCAGGTGGCTG 1

RESULT 36
US-10-310-914A-1045310/c
; Sequence 1045310, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045310
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045310

Query Match      1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1274 CTGTGGGAGAGGCTTAGACCTG 1295
|||||
```

Db 22 CTGTGGGAGAGGCTTACACCTG 1

RESULT 37

US-10-310-914A-1045313/c
; Sequence 1045313, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045313

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1045313

Query Match 1.3%; Score 22; DB 8; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.99;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1468 GAGTAGGCATTACCTTCTGGG 1489

Db 22 GAGTAGGCATTACCTTCTGGG 1

RESULT 38

US-10-310-914A-1045314/c
; Sequence 1045314, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045314

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1045314

Query Match 1.3%; Score 22; DB 8; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.99;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1343 GGACCATGTGCATTTCACCTGGG 1364

Db 22 GGACCATGTGCATTTCACCTGGG 1

RESULT 39

US-10-310-914A-1045315/c
; Sequence 1045315, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045315

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1045315

Query Match 1.3%; Score 22; DB 8; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.99;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 TTCTATTGGGGGTGGCAGGG 1614

Db 22 TTCTATTGGGGGTGGCAGGG 1

RESULT 40

US-10-310-914A-1045319/c
; Sequence 1045319, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045319

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1045319

Query Match 1.3%; Score 22; DB 8; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.99;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 CAGGGCCCTTCCTTCCTGCTC 1433

Db 22 CAGGGCCCTTCCTTCCTGCTC 1

RESULT 41

US-10-310-914A-1045323/c
; Sequence 1045323, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045323

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1045323

Query Match 1.3%; Score 22; DB 8; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.99;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1407 CCTGCCAGGGCCCTTCCTTCC 1428

Db 22 CCTGCCAGGGCCCTTCCTTCC 1

```
RESULT 42
US-10-310-914A-1045324/c
; Sequence 1045324, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045324
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045324
Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1362 GGGCCATGGGACTACATCTCC 1383
Db 22 GGGCCATGGGACTACATCTCC 1

RESULT 43
US-10-310-914A-1045329/c
; Sequence 1045329, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045329
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045329
Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1439 CTTCCAGTGGCCTGATCATGGA 1460
Db 22 CTTCCAGTGGCCTGATCATGGA 1

RESULT 44
US-10-310-914A-1045330/c
; Sequence 1045330, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045330
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045330
Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1212 AGCTGCCACACCTTTCTGGGA 1233
Db 22 AGCTGCCACACCTTTCTGGGA 1

RESULT 45
US-10-310-914A-1045332/c
; Sequence 1045332, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045332
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045332
Query Match 1.3%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1392 CCAGCTGGTCTGATCCCTGCCA 1413
Db 22 CCAGCTGGTCTGATCCCTGCCA 1

RESULT 46
US-10-310-914A-1045305/c
; Sequence 1045305, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045305
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045305
Query Match 1.2%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1604 GGTGGCAGGCGCCACTCTAT 1624
Db 21 GGTGGCAGGCGCCACTCTAT 1
```

RESULT 47

US-10-310-914A-1045333/c
; Sequence 1045333, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045333
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045333

Query Match 1.2%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 CCCTATTGCCACCTAACCA 1529
Db 21 CCCTATTGCCACCTAACCA 1

RESULT 48

US-11-234-786-293
; Sequence 293, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; TITLE OF INVENTION: POLYPEPTIDES THEREOF
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234.786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453

; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-234-786-293

Query Match 1.2%; Score 21; DB 12; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGCGCGACACGC 1713
Db 232 GTACCTCGCGCGACACGC 252

RESULT 49

US-11-116-881A-2005
; Sequence 2005, Application US/11116881A
; Publication No. US2006004194A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116.881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2005
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-11-116-881A-2005

Query Match 1.2%; Score 21; DB 9; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACCTCGCGCGACACGC 1713
Db 283 GTACCTCGCGCGACACGC 303

RESULT 50

US-11-116-881A-992
; Sequence 992, Application US/11116881A

```
Query Match      1.2%; Score 21; DB 9; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 21; Conservative 0; Mismatches 0; Indels
```

```

RESULT 53
US-11-206-587-4/c
; Sequence 4, Application US/11206587
; Publication No. US20060040306A1
; GENERAL INFORMATION:
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
; TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 381552004900
; CURRENT APPLICATION NUMBER: US/11/206,587
; CURRENT FILING DATE: 2005-08-18
; PRIOR APPLICATION NUMBER: US/10/012,140
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: 60/246,768
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,772
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,185
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1820
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (146)...(1390)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1820)
; OTHER INFORMATION: n = A,T,C or G
US-11-206-587-4

Query Match
Best Local Similarity 100.0%; Score 21; DB 9; Length 1820;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 GTACTCGCGCGGACACGC 1713
DB 27 GTACTCGCGCGGACACGC 7

RESULT 54
US-10-310-914A-1045308/c
; Sequence 1045308, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045308
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045308

Query Match
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 GCCACTCTGGCTCTCTCTG 1322
DB 20 GCCACTCTGGCTCTCTCTG 1

RESULT 55
US-10-310-914A-1045312/c
; Sequence 1045312, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045312
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045312

Query Match
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1418 CCTTCCTCTCTCTCTCTG 1437
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DB 20 CCTTCCTCTCTCTCTCTG 1

RESULT 56
US-11-136-527-193835/c
; Sequence 193835, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193835
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-193835

Query Match
Best Local Similarity 100.0%; Score 20; DB 12; Length 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCTCTGCTGCAAGGAG 570
DB 24 CGGACTCTCTGCTGCAAGGAG 5

RESULT 57
US-11-136-527-193843/c
; Sequence 193843, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193843
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-193843

Query Match
Best Local Similarity 100.0%; Score 20; DB 12; Length 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCTCTGCTGCAAGGAG 570
DB 20 CGGACTCTCTGCTGCAAGGAG 1

RESULT 58
US-11-136-527-193849/c
; Sequence 193849, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193849
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-193849

Query Match          1.2%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCCTGCTGCAAGGAG 570
Db 21 CGGACTCCTGCTGCAAGGAG 2

RESULT 59
US-11-136-527-193854/c
; Sequence 193854, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193854
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-193854

Query Match          1.2%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCCTGCTGCAAGGAG 570
Db 23 CGGACTCCTGCTGCAAGGAG 4

RESULT 60
US-11-031-356-14/c
; Sequence 14, Application US/11031356
; Publication No. US20050272056A1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech Inc.
; APPLICANT: Deiss et al., Louis. P.
; TITLE OF INVENTION: Gene Identification Method
; FILE REFERENCE: 65507-F / 003/PTI-US4
; CURRENT APPLICATION NUMBER: US/11/031,356
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 10/704,112
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 09/499,553
```

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; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/284,782
; PRIOR FILING DATE: 1993-07-06
; PRIOR APPLICATION NUMBER: 6,057,111
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: PCT/US97/20989
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/030,549
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Primer
US-11-031-356-14

Query Match          1.2%; Score 20; DB 12; Length 43;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1694 TACCTCGCGCGGACCACGC 1713
Db 43 TACCTCGCGCGGACCACGC 24

RESULT 61
US-09-925-065A-613855/c
; Sequence 613855, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 613855
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 481, 482, 483, 484, 485, 486
; OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-613855

Query Match          1.2%; Score 20; DB 6; Length 486;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1101 TTATGGAGCTCCAGGGTACC 1120
Db 251 TTATGGAGCTCCAGGGTACC 232

RESULT 62
US-11-136-527-3780/c
; Sequence 3780, Application US/11136527
```

```
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3780
; LENGTH: 680
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7876

Query Match      1.2%; Score 20; DB 12; Length 680;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCCTCTGCTCAAGGAG 570
DB 238 CGGACTCCTCTGCTCAAGGAG 219

RESULT 63
US-11-136-527-7876/c
; Sequence 7876, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7876
; LENGTH: 680
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7876

Query Match      1.2%; Score 20; DB 12; Length 680;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCCTCTGCTCAAGGAG 570
DB 238 CGGACTCCTCTGCTCAAGGAG 219

RESULT 64
US-10-750-185-36767/c
; Sequence 36767, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
```

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; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36767
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Bovine 19866880507628
US-10-750-185-36767

Query Match      1.2%; Score 20; DB 8; Length 993;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1312 GGCTCCTCTGCTTGGCTG 1331
DB 892 GGCTCCTCTGCTTGGCTG 873

RESULT 65
US-10-750-623-36767/c
; Sequence 36767, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36767
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Bovine 19866880507628
US-10-750-623-36767

Query Match      1.2%; Score 20; DB 8; Length 993;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1312 GGCTCCTCTGCTTGGCTG 1331
DB 892 GGCTCCTCTGCTTGGCTG 873

RESULT 66
US-11-096-568A-25683/c
; Sequence 25683, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25683
; LENGTH: 1280
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1280)
```



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; OTHER INFORMATION: Ceres Seq. ID no. 13492847
US-11-096-568A-25683

Query Match          1.2%; Score 20; DB 9; Length 1280;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GGCAGCAGCTTCAGCTACCC 485
Db 510 GGCAGCAGCTTCAGCTACCC 491

RESULT 67
US-11-136-527-3889
; Sequence 3889, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3889
; LENGTH: 13894
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3889

Query Match          1.2%; Score 20; DB 12; Length 13894;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 CGGACTCTCGTGCAAGGAG 570
Db 3394 CGGACTCTCGTGCAAGGAG 3413

RESULT 68
US-10-310-914A-1045321/c
; Sequence 1045321, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045321
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045321

Query Match          1.1%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1225 TTCTGGGAGAGCATGGC 1243
Db 19 TTCTGGGAGAGCATGGC 1

RESULT 69
US-10-310-914A-1045325/c
; Sequence 1045325, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045325
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045325
```

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; Sequence 1045325, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045325
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045325

Query Match          1.1%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 ACCTTCTGGGAGTGAACCC 1498
Db 19 ACCTTCTGGGAGTGAACCC 1

RESULT 70
US-10-310-914A-1045331/c
; Sequence 1045331, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045331
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045331

Query Match          1.1%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1201 CTGCCAGGCCGAGCTGCCA 1219
Db 19 CTGCCAGGCCGAGCTGCCA 1

RESULT 71
US-10-310-914A-1045334/c
; Sequence 1045334, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045334
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045334
```

```
; ORGANISM: Human
US-10-310-914A-1045334

Query Match      1.1%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 GCCAGGCCCGAGTGCACCA 1221
DB 19 GCCAGGCCCGAGTGCACCA 1

RESULT 72
US-10-310-914A-1045335/c
; Sequence 1045335, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045335
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045335

Query Match      1.1%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 GCCAGGCCCGAGTGCACCA 1221
DB 19 GCCAGGCCCGAGTGCACCA 1

RESULT 73
US-11-101-244-1430754
; Sequence 1430754, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430754
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430754

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 35;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 81 GGAGACATATGATAAACCA 99
```

```
DB 1 GGAGACAUAGUAUAAACCA 19

RESULT 74
US-11-101-244-1430755
; Sequence 1430755, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430755
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430755

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 35;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 497 TCAAGGCATCCCTGTGTA 515
DB 1 UCAAGGCATCCCTGTGTA 515

RESULT 75
US-11-101-244-1430756
; Sequence 1430756, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430756
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430756

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 52.6%; Pred. No. 35;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1655 GCTGATGTTCTGTATCTTA 1673
```

Db 1 GCUGAUGUUCUGUAUCUUA 19

RESULT 76

US-11-101-244-1430757
; Sequence 1430757, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430757
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430757

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 35;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 767 TCGAGCTGGCCCAAGTG 785

Db 1 UCGAUGCGUGGCCAAGUG 19

RESULT 77

US-11-101-244-1430758
; Sequence 1430758, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430758
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430758

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 35;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1455 CATGAAAGTAAGGAGTTA 1473

Db 1 CAUGGAAAGUAGGAGUUA 19

RESULT 78

US-11-101-244-1430759
; Sequence 1430759, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430759
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430759

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 35;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 808 GAGAGACCAGTAAGATCT 826

Db 1 GAGAGACCAGUAAGAUCU 19

RESULT 79

US-11-101-244-1430760
; Sequence 1430760, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430760
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430760

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 35;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1678 GACCACAGTTTGAAGTAC 1696

Db 1 GACCACAGUUGUAAGUAC 19

masses II; conservative 0; matches 0; index 0; gaps 0;

RESULT 84

Query Match	1.1%	Score 19;	DB 10;	Length 19;
Best Local Similarity	57.9%;	Pred. No. 35;		
Matches 11;	Conservative	8;	Mismatches	0;
			Indels	0;
			Gaps	0;

Query Match	1.1%	Score 19;	DB 10;	Length 19;
Best Local Similarity	78.9%	Pred. No. 35;		
Matches	15;	Conservative	4;	Mismatches 0; Indels 0; Gaps 0;
QY	163	CCAGAGAGCATTACCTTCA	181	
Db	1	CCAGAGAGCAUUAACCUCA	19	

```
US-11-101-244-1430765
; Sequence 1430765, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430765
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430765

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 68.4%; Pred. No. 35;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1677 TGACCACAGTTTGTGAAGTA 1695
Db 1 UGACCACAGUUUGUAGUA 19

RESULT 85
US-11-101-244-1430766
; Sequence 1430766, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430766
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430766

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 52.6%; Pred. No. 35;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GTTCTTGGCTGATGTTCTG 1666
Db 1 GUUCUUGGCGUGAUGUUCUG 19

RESULT 86
US-11-101-244-1430767
; Sequence 1430767, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430767
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430767

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 35;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1524 TAACCAATCATGCAAACTT 1542
Db 1 UAACCAAUCAUGCAAAACUU 19

RESULT 87
US-11-101-244-1430768
; Sequence 1430768, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430768
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430768

Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 73.7%; Pred. No. 35;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1524 TAACCAATCATGCAAACTT 1542
Db 1 UAACCAAUCAUGCAAAACUU 19

RESULT 88
US-11-101-244-1430769
; Sequence 1430769, Application US/11101244
```

RESULT 92
US-11-101-244-1430773
; Sequence 1430773, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430773
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430773

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 35;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1279 GGAGAGGCTTAGACCTGAA 1297
|||||:|:|:|:|:|:|:|:|:|:|
Db 1 GGAGAGGCUUAGACCUGAA 19

RESULT 93
US-11-101-244-1430774
; Sequence 1430774, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430774
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430774

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 35;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 829 GACCTTATCAGCAGCATCA 847
|||||:|:|:|:|:|:|:|:|:|:|
Db 1 GACCUUUAUCGACGACAUCA 19

RESULT 94
US-11-101-244-1430775
; Sequence 1430775, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430775
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430775

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 52.6%; Pred. No. 35;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1656 CTGATGTTCTGTATCTTAA 1674
|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 CUGAUGUUCUGUAUCUAAA 19

RESULT 95
US-11-101-244-1430776
; Sequence 1430776, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430776
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430776

Query Match 1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 35;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1235 AAGCATGGCCTACAGAATG 1253
|||||:|:|:|:|:|:|:|:|:|:|
Db 1 AAGCAUGGCCUACAGNAUG 19

RESULT 96
US-11-101-244-1430777
; Sequence 1430777, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

<p>; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101,244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 1430777 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-1430777</p>	<p>Query Match 1.1%; Score 19; DB 10; Length 19; Best Local Similarity 52.6%; Pred. No. 35; Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;</p>	<p>QY 1635 GGAGTTGGTCTGCTTCCT 1653 :: :: :: :: : Db 1 GGAGUUGGUUCUGGUUCUU 19</p>
<p>RESULT 97 US-11-101-244-1430778 ; Sequence 1430778, Application US/11101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmakon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101,244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 1430778 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-1430778</p>	<p>Query Match 1.1%; Score 19; DB 10; Length 19; Best Local Similarity 89.5%; Pred. No. 35; Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;</p>	<p>QY 141 CAAGGACCCCTGCCACCAT 159 :: :: :: :: : Db 1 CAAGGACCCCTGCCACCAU 19</p>
<p>RESULT 98 US-11-101-244-1430780 ; Sequence 1430780, Application US/11101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmakon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101,244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 1430780 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-1430780</p>	<p>Query Match 1.1%; Score 19; DB 10; Length 19; Best Local Similarity 73.7%; Pred. No. 35; Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;</p>	<p>QY 1609 GCAGGGCCCCTCTATGTT 1627 :: :: :: :: : Db 1 GCAGGGCCCCTCTATGTT 19</p>
<p>RESULT 99 US-11-101-244-1430781 ; Sequence 1430781, Application US/11101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmakon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101,244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 1430781 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-1430781</p>	<p>Query Match 1.1%; Score 19; DB 10; Length 19; Best Local Similarity 63.2%; Pred. No. 35; Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;</p>	<p>QY 168 GAGCATTACCTTCATCTCT 186 :: :: :: :: : Db 1 GAGCAUUAUCCUUAUCUCU 19</p>
<p>RESULT 100 US-11-101-244-1430782 ; Sequence 1430782, Application US/11101244 ; Publication No. US20050246794A1 ; GENERAL INFORMATION: ; APPLICANT: Dharmakon, Inc. ; APPLICANT: Khvorova, Anastasia ; APPLICANT: Reynolds, Angela ; APPLICANT: Leake, Devin ; APPLICANT: Marshall, William ; APPLICANT: Scaringe, Stephen ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA ; FILE REFERENCE: 13499US ; CURRENT APPLICATION NUMBER: US/11/101,244 ; CURRENT FILING DATE: 2005-04-07 ; PRIOR APPLICATION NUMBER: 60/502,050 ; PRIOR FILING DATE: 2003-09-10 ; PRIOR APPLICATION NUMBER: 60/426,137 ; PRIOR FILING DATE: 2002-11-14 ; NUMBER OF SEQ ID NOS: 1591911 ; SOFTWARE: Proprietary ; SEQ ID NO 1430782 ; LENGTH: 19 ; TYPE: RNA ; ORGANISM: Homo sapiens US-11-101-244-1430782</p>	<p>Query Match 1.1%; Score 19; DB 10; Length 19; Best Local Similarity 73.7%; Pred. No. 35; Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;</p>	<p>QY 1609 GCAGGGCCCCTCTATGTT 1627 :: :: :: :: : Db 1 GCAGGGCCCCTCTATGTT 19</p>

Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
US-11-101-244-1430778	1.1%	52.6%	19	10	0	0	0
<p>Query Match</p> <p>Best Local Similarity 52.6%; Pred. No. 35;</p> <p>Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;</p>							
QY 1635	GGAGTTGGTCTGCTTCTT	1653					
DB 1	GGAGUUGGUUCUGGUUCU	19					
<p>RESULT 97</p> <p>US-11-101-244-1430778</p> <p>; Sequence 1430778, Application US/11101244</p> <p>; Publication No. US20050246794A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Dharmacon, Inc.</p> <p>; APPLICANT: Khvorova, Anastasia</p> <p>; APPLICANT: Reynolds, Angela</p> <p>; APPLICANT: Leake, Devin</p> <p>; APPLICANT: Marshall, William</p> <p>; APPLICANT: Scaringe, Stephen</p> <p>; TITLE OF INVENTION: Functional and Hyperfunctional siRNA</p> <p>; FILE REFERENCE: 13499US</p> <p>; CURRENT APPLICATION NUMBER: US/11/101,244</p> <p>; CURRENT FILING DATE: 2005-04-07</p> <p>; PRIOR APPLICATION NUMBER: 60/502,050</p> <p>; PRIOR FILING DATE: 2003-09-10</p> <p>; PRIOR APPLICATION NUMBER: 60/426,137</p> <p>; PRIOR FILING DATE: 2002-11-14</p> <p>; NUMBER OF SEQ ID NOS: 1591911</p> <p>; SOFTWARE: Proprietary</p> <p>; SEQ ID NO 1430777</p> <p>; LENGTH: 19</p> <p>; TYPE: RNA</p> <p>; ORGANISM: Homo sapiens</p>							
<p>US-11-101-244-1430778</p> <p>Query Match</p> <p>Best Local Similarity 1.1%; Score 19; DB 10; Length 19;</p> <p>Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;</p>							
QY 1635	GGAGTTGGTCTGCTTCTT	1653					
DB 1	GGAGUUGGUUCUGGUUCU	19					
<p>RESULT 98</p> <p>US-11-101-244-1430780</p> <p>; Sequence 1430780, Application US/11101244</p> <p>; Publication No. US20050246794A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Dharmacon, Inc.</p> <p>; APPLICANT: Khvorova, Anastasia</p> <p>; APPLICANT: Reynolds, Angela</p> <p>; APPLICANT: Leake, Devin</p> <p>; APPLICANT: Marshall, William</p> <p>; APPLICANT: Scaringe, Stephen</p> <p>; TITLE OF INVENTION: Functional and Hyperfunctional siRNA</p> <p>; FILE REFERENCE: 13499US</p> <p>; CURRENT APPLICATION NUMBER: US/11/101,244</p> <p>; CURRENT FILING DATE: 2005-04-07</p> <p>; PRIOR APPLICATION NUMBER: 60/502,050</p> <p>; PRIOR FILING DATE: 2003-09-10</p> <p>; PRIOR APPLICATION NUMBER: 60/426,137</p> <p>; PRIOR FILING DATE: 2002-11-14</p> <p>; NUMBER OF SEQ ID NOS: 1591911</p> <p>; SOFTWARE: Proprietary</p> <p>; SEQ ID NO 1430778</p> <p>; LENGTH: 19</p> <p>; TYPE: RNA</p> <p>; ORGANISM: Homo sapiens</p>							
<p>US-11-101-244-1430778</p> <p>Query Match</p> <p>Best Local Similarity 1.1%; Score 19; DB 10; Length 19;</p> <p>Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;</p>							
QY 141	CAAGGACCCCTGGCCACCAT	159					
DB 1	CAAGGACCCCTGGCCACCAU	19					
<p>RESULT 99</p> <p>US-11-101-244-1430781</p> <p>; Sequence 1430781, Application US/11101244</p> <p>; Publication No. US20050246794A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Dharmacon, Inc.</p> <p>; APPLICANT: Khvorova, Anastasia</p> <p>; APPLICANT: Reynolds, Angela</p> <p>; APPLICANT: Leake, Devin</p> <p>; APPLICANT: Marshall, William</p> <p>; APPLICANT: Scaringe, Stephen</p> <p>; TITLE OF INVENTION: Functional and Hyperfunctional siRNA</p> <p>; FILE REFERENCE: 13499US</p> <p>; CURRENT APPLICATION NUMBER: US/11/101,244</p> <p>; CURRENT FILING DATE: 2005-04-07</p> <p>; PRIOR APPLICATION NUMBER: 60/502,050</p> <p>; PRIOR FILING DATE: 2003-09-10</p> <p>; PRIOR APPLICATION NUMBER: 60/426,137</p> <p>; PRIOR FILING DATE: 2002-11-14</p> <p>; NUMBER OF SEQ ID NOS: 1591911</p> <p>; SOFTWARE: Proprietary</p> <p>; SEQ ID NO 1430781</p> <p>; LENGTH: 19</p> <p>; TYPE: RNA</p> <p>; ORGANISM: Homo sapiens</p>							
<p>US-11-101-244-1430781</p> <p>Query Match</p> <p>Best Local Similarity 1.1%; Score 19; DB 10; Length 19;</p> <p>Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;</p>							
QY 1609	GCAGGCCCTCTATGTT	1627					
DB 1	GCAGGCCCTCTATGTT	19					
<p>RESULT 100</p> <p>US-11-101-244-1430782</p> <p>; Sequence 1430782, Application US/11101244</p> <p>; Publication No. US20050246794A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Dharmacon, Inc.</p> <p>; APPLICANT: Khvorova, Anastasia</p> <p>; APPLICANT: Reynolds, Angela</p> <p>; APPLICANT: Leake, Devin</p>							


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; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1430782
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430782

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Query Match      1.1%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 35;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY      1447  GGCCTGATCATGGAAAGTA 1465
           |||:|:|:|:|:|:|:|:|
Db       1  GGCCUGAUGGAAAGUA 19

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Search completed: March 11, 2006, 21:14:34
Job time : 685 secs